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Mpsrch_pp      protein - protein database search, using Smith-Waterman algorithm
Run on:        Mon Jun 19 15:54:15 2000;      MspPar time 5.82 Seconds
Tabular output not generated.                  325,701 Million cell updates/sec

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Title:	>US-09-142-524A-1
Description:	(1-80) from US09142524A.pep
Perfect Score:	569
Sequence:	1 MKVTVAFNQFGPNRRVFYIKR...

Scoring table: PAM 150  
Gap 11

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: ~~a-geneseq35~~  
1:geneseqp

Statistics: Mean 27.708; Variance 116.071; scale 0.239

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	569	100.0	80	1	W21370	Multi-epitope peptide	5.38e-45
2	372	65.4	105	1	W27370	Multi-epitope peptide	1.34e-25
3	372	65.4	134	1	W27371	Multi-epitope peptide	1.34e-25
4	129	22.7	460	1	R65791	Japanicum allergen	6.23e-03
5	129	22.7	514	1	R53690	Japanese cedar pollen	6.23e-03
6	129	22.7	514	1	R73330	Japanese cedar pollen	6.23e-03
7	139	22.7	514	1	R93399	Japanese cedar pollen	6.23e-03
8	139	22.7	514	1	R65792	Japan cedar pollen Cry	6.23e-03
9	139	22.7	514	1	R15866	Japanicum allergen.	6.23e-03
10	128	20.6	47	1	W80357	Cedar pollen allergen	7.58e-03
11	117	20.6	17	1	W80347	Sugi allergen protein	6.45e-02
12	117	20.6	33	1	W80339	Sugi allergen protein	6.45e-02
13	115	20.2	17	1	R15862	Sugi allergen protein	9.47e-02
14	111	19.5	17	1	W80345	Cedar pollen allergen	2.03e-01
15	111	19.5	17	1	R15880	Sugi allergen protein	2.03e-01
16	107	18.8	15	1	R37884	Cedar pollen allergen	4.34e-01
17	107	18.8	15	1	W57760	Japan cedar pollen mat	4.34e-01
18	107	18.8	47	1	W80356	Residues 66-80 of Cry	4.34e-01
19	106	18.6	47	1	W80356	Sugi allergen protein	5.24e-01
20	103	18.1	35	1	W57764	Sugi allergen protein	5.20e-01
21	98	17.2	15	1	R37968	Residues 186-200 of Cr	2.33e+00
22	98	17.2	15	1	R37968	Japan cedar pollen mat	2.33e+00
23	98	17.2	15	1	R37907	Japan cedar pollen mat	2.33e+00

24	98	17.2	15	1	M57763	Residues 181-195 of Cr	2.33e+00
25	97	17.0	30	1	R35568	Cry j I pollen allergen	2.80e+00
26	97	17.0	354	1	W04314	Chamaecyparis obtusa p	2.80e+00
27	97	17.0	354	1	W42121	Japanese cypress polle	2.80e+00
28	97	17.0	375	1	W04345	Chamaecyparis obtusa p	2.80e+00
29	97	17.0	514	1	W04346	Chamaecyparis obtusa p	2.80e+00
30	97	17.0	514	1	W42122	Japanese cypress polle	2.80e+00
31	95	16.7	15	1	M57765	Residues 211-225 of Cr	4.03e+00
32	95	16.7	15	1	M57765	Residues 211-225 of Cr	4.03e+00
33	95	16.7	15	1	R89293	Japanese cedar pollen	4.03e+00
34	95	16.7	17	1	W80349	Sugi allergen protein	4.03e+00
35	95	16.7	20	1	R45563	Cry j I pollen allergen	4.03e+00
36	95	16.7	20	1	R82512	Cry j I Japanese cedar	4.03e+00
37	95	16.7	26	1	R45594	Cry j I pollen allergen	4.03e+00
38	95	16.7	28	1	R45560	Cry j I pollen allergen	4.03e+00
39	95	16.7	30	1	W44687	T-cell epitope peptide	4.03e+00
40	95	16.7	353	1	R75388	Japanese cedar pollen	4.03e+00
41	95	16.7	367	1	R45577	Jun s I.	4.03e+00
42	95	16.7	374	1	R45541	Cry j I pollen allergen	4.03e+00
43	95	16.7	374	1	R60166	Japanese cedar pollen	4.03e+00
44	95	16.7	374	1	R31937	Cry j I.	4.03e+00
45	95	16.7	680	1	R34445	Sequence encoded by a	4.03e+00
46	95	16.7	680	1	W49015	Human K $\alpha$ l protein.	4.03e+00

## ALIGNMENTS

RESULT	1
ID	W27369 standard; peptide; 80 AA.
AC	W27369.

Page 7

24-MAR-1998 (first entry)  
DE Multi-epitope peptide used as immunotherapeutic agent #2.  
KW Multi-epitope peptide; immunotherapeutic agent; allergic disease;  
T-cell epitope region; allergen; lymphocyte; immunoglobulin E.  
OS Synthetic.  
PN WO9732600-A1.  
PD 12-SEP-1997.  
PF 10-MAR-1997; J00740.  
PR 10-MAR-1996; JP-080702.  
PA (MEIP) MEIJI MILK PROD CO LTD.  
PI Dairiki K, Iwama A, Kino K, Kume A, Sone T;  
DR WPI: 97-470495/43.  
PT Peptide immuno:therapeutic agent to treat allergic diseases -  
PT contains multi-epitope peptide containing T cell epitope regions  
from different allergens  
PS Claim 6: Page 31: 58pp; Japanese.  
CC The present sequence represents a multi-epitope peptide which is used as  
a new immunotherapeutic agent. It comprises T cell epitope regions from 2  
or more different allergens (preferably linked via arginine or lysine  
dimers), where the T cell epitope regions have a positively index  
greater than 100 as measured in a patient group responding to the  
allergen: have at least 70% reactivity with lymphocytes from patients  
responding to the allergen: and are not reactive with immunoglobulin E  
(IgE) antibodies from patients responsive to the allergen. The agent can  
be used to prevent and treat a wide variety of allergic diseases, e.g. by  
desensitisation. Side effects, e.g. those mediated by IgE, are reduced.  
SQ Sequence 105 AA;

Query Match 65.4%; Score 372; DB 1; Length 105;  
Best Local Similarity 100.0%; Pred. No. 1,34e-25;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MKVTVAENFGPNRRVFIKRVSNVLIHGRRIDIFASKNFHLQKNTIGTGR 51  
QY 1 MKVTVAENFGPNRRVFIKRVSNVLIHGRRIDIFASKNFHLQKNTIGTGR 51

RESULT 3  
ID W27371 standard; peptide; 134 AA.  
AC W27371;  
DT 24-MAR-1998 (first entry)  
DE Multi-epitope peptide used as immunotherapeutic agent #3.  
KW Multi-epitope peptide; immunotherapeutic agent; allergic disease;  
T-cell epitope region; allergen; lymphocyte; immunoglobulin E.  
OS Synthetic.  
PN WO9732600-A1.  
PD 12-SEP-1997.  
PF 10-MAR-1997; J00740.  
PR 10-MAR-1996; JP-080702.  
PA (MEIP) MEIJI MILK PROD CO LTD.  
PI Dairiki K, Iwama A, Kino K, Kume A, Sone T;  
DR WPI: 97-470495/43.  
PT Peptide immuno:therapeutic agent to treat allergic diseases -  
PT contains multi-epitope peptide containing T cell epitope regions  
from different allergens  
PS Claim 6: Page 32: 58pp; Japanese.  
CC The present sequence represents a multi-epitope peptide which is used as  
a new immunotherapeutic agent. It comprises T cell epitope regions from 2  
or more different allergens (preferably linked via arginine or lysine  
dimers), where the T cell epitope regions have a positively index  
greater than 100 as measured in a patient group responding to the  
allergen: have at least 70% reactivity with lymphocytes from patients  
responding to the allergen: and are not reactive with immunoglobulin E  
(IgE) antibodies from patients responsive to the allergen. The agent can  
be used to prevent and treat a wide variety of allergic diseases, e.g. by  
desensitisation. Side effects, e.g. those mediated by IgE, are reduced.  
SQ Sequence 134 AA;

Query Match 65.4%; Score 372; DB 1; Length 134;  
Best Local Similarity 100.0%; Pred. No. 1,34e-25;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MKVTVAENFGPNRRVFIKRVSNVLIHGRRIDIFASKNFHLQKNTIGTGR 51

QY 1 MKVTVAENFGPNRRVFIKRVSNVLIHGRRIDIFASKNFHLQKNTIGTGR 51

RESULT 4  
ID R69791 standard; Protein; 460 AA.  
AC R69791;  
DT 27-SEP-1995 (first entry)  
DE Japonicum allergen residues 55-514.  
KW Japonicum allergen; residues 55-514; induced histamine release;  
antiallergic peptide; IgE cross-linking inhibition.  
OS Japonicum SP.  
PN WO9502412-A.  
PD 26-JAN-1995.  
PF 15-JUL-1994; J01164.  
PR 16-JUL-1993; JP-177008.  
PR 01-SEP-1993; JP-217725.  
PR 07-APR-1994; JP-069336.  
PA (MEIP) MEIJI MILK PROD CO LTD.  
PI Kino K, Kohno Y, Komiyama N, Sone T;  
DR WPI: 95-067159/09.  
DR N-PSDB; Q84044.  
PT Peptide antiallergic agent - inhibits cross-linking of allergen  
with IgE antibody  
PS Disclosure; Pages 26-27; 46pp; Japanese.  
CC O84044 encodes R69791 Japonicum allergen residues 55-514, from  
which the antiallergic peptides R69845-R69809 were derived.  
CC The peptides ability to inhibit the cross-linking of an allergen,  
to an IgE antibody can be used in the prevention and treatment of  
allergic diseases.  
SQ Sequence 460 AA;

Query Match 22.7%; Score 129; DB 1; Length 460;  
Best Local Similarity 100.0%; Pred. No. 6,23e-03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 182 IDIFASKNFHLQKNTIGTG 200  
QY 31 IDIFASKNFHLQKNTIGTG 49

RESULT 5  
ID R53690 standard; Protein; 514 AA.  
AC R53690;  
DT 01-FEB-1995 (first entry)  
DE Japanese cedar pollen allergen Cry j II.  
KW Cedar pollinosis; diagnostic.  
OS Cryptomeria japonica.  
PN WO9411512-A.  
PD 26-MAY-1994.  
PF 12-NOV-1993; U11000.  
PR 12-NOV-1992; US-975179.  
PA (IMMU-) IMMUNOLOGIC PHARM CORP.  
PI Brauer A, Kuo M, Pollock J, Yeung S;  
DR WPI: 94-183513/22.  
DR N-PSDB; Q66048.  
PT Allergenic Cry j II protein and fragments from Japanese cedar  
PT pollen - used to diagnose, treat and prevent Japanese cedar  
PT pollinosis  
PS Claim 2: Fig 4; 89pp; English.  
CC The sequence is of a Japanese cedar pollen allergen Cry j  
II. The protein and its fragments can be used for diagnosis and  
treatment of Japanese cedar pollinosis and to identify similar  
sequences in other plants.  
CC See also R53692-6.  
SQ Sequence 514 AA;

Query Match 22.7%; Score 129; DB 1; Length 514;  
Best Local Similarity 100.0%; Pred. No. 6,23e-03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 IDIFASKNFHLQKNTIGTG 254

OYJ 31 IDIFASKNFHLQKNTIGTG 49

## RESULT 6

ID R74333 standard; Protein; 514 AA.  
AC R74333;  
DE 01-NOV-1995 (first entry)  
KW Japanese cedar pollen allergen.  
KW Japanese cedar; pollen; allergen; allergy; therapy; diagnostic;  
KW desensitizer.  
OS Cryptomeria japonica.  
PN EP-655500-A.  
PD 31-MAY-1995.  
PE 03-NOV-1994; 308117.  
PR 05-NOV-1993; JP-299151.  
PR 20-DEC-1993; JP-344596.  
PR 27-DEC-1993; JP-346814.  
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.  
PI Kurimoto M, Namba M, Torioge K;  
DR WPI: 95-195588/26.  
DR N-PSDB: 090156.  
PT New Japanese cedar pollen allergen polypeptide - and DNA coding for it,  
PT useful for treatment and diagnosis of cedar pollen allergy  
PS Claim 5; Page 26-28; 41pp; English.  
CC The gene encoding an allergen of Japanese cedar pollen was isolated  
CC by PCR amplification using primers based on portions of the allergen  
CC protein. The gene was used for recombinant allergen production in  
CC E. coli (vector plasmid pKK-223-3).  
SQ Sequence 514 AA;

## Query Match

Best Local Similarity 100.0%; Pred. No. 6.23e-03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 236 IDIFASKNFHLQKNTIGTG 254

OY 31 IDIFASKNFHLQKNTIGTG 49

## RESULT 7

ID R93599 standard; Protein; 514 AA.  
AC R93599;  
DE 16-AUG-1996 (first entry)  
KW Japan cedar pollen Cry j II allergen.  
KW Allergen; epitope; overlapping peptide; Cry j II; cedar pollen;  
KW Sugi pollinosis; diagnosis; treatment.  
OS Cryptomeria japonica.  
FH Key location/Qualifiers  
FT peptide 1..54  
FT protein /\*label= sig\_peptide  
FT /\*label= 55..514  
FT /\*label= mat\_protein

J08047392-A.

20-FEB-1996.

07-NOV-1994; 297840.

05-NOV-1993; JP-276773.

26-MAY-1994; JP-134868.

(MEIP) MEIJI MILK PROD CO LTD.

WPI: 96-166249/17.

N-PSDB: T18102.

Japan cedar pollen allergen Cry j II epitope - comprises at least

part of specified 460 amino acid protein

Claim 1; Page 10-11; 17pp; Japanese.

R93599 is a Japan cedar pollen Cry j II allergen which is useful

in the diagnosis, prevention and treatment of Sugi pollinosis,

the allergic reaction to Japan cedar pollen. Significant regions of

the allergen were identified using overlapping peptides of the full

epitope derived from a Cry j II antigen-specific T cell line

(see R9781-1-997860). Amino acids 66-80 (R97884) and 186-200 (R978908)

of the full mature 460 amino acid allergen are the most allergenic

of the 90 peptides tested.

Sequence 514 AA;

Query Match 22.7%; Score 129; DB 1; Length 514;  
Best Local Similarity 100.0%; Pred. No. 6.23e-03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 236 IDIFASKNFHLQKNTIGTG 254

OY 31 IDIFASKNFHLQKNTIGTG 49

## RESULT 8

ID R69792 standard; Protein; 514 AA.  
AC R69792;  
DE 27-SEP-1995 (first entry)  
KW Japonicum allergen.  
KW Japonicum allergen; induced histamine release; antiallergic peptide;  
KW Ige cross-linking inhibition.  
OS Japonicum sp.  
PN WO9502412-A.  
PD 26-JAN-1995.  
PE 15-JUL-1994; J01164.  
PR 16-JUL-1993; JP-177008.  
PR 01-SEP-1993; JP-217725.  
PR 07-APR-1994; JP-069336.  
PA (MEIP) MEIJI MILK PROD CO LTD.  
PI Kino K, Kohno Y, Komiyama N, Sone T;  
DR WPI: 95-067159/09.  
DR N-PSDB: 084045, 084046.  
PT Peptide anti-allergic agent - inhibits cross-linking of allergen  
PT with Ige antibody  
PS Example 3; Pages 27-28; 46pp; Japanese.  
CC 084045 encodes R69792 Japonicum allergen, from which the antiallergic  
CC peptides R69845-R69809 were derived. The peptides ability to inhibit  
CC the cross-linking of an allergen, to an Ige antibody can be used in  
CC the prevention and treatment of allergic diseases.  
SQ Sequence 514 AA;

## Query Match

Best Local Similarity 100.0%; Pred. No. 6.23e-03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 236 IDIFASKNFHLQKNTIGTG 254

OY 31 IDIFASKNFHLQKNTIGTG 49

## RESULT 9

ID R81586 standard; Protein; 514 AA.

AC R81586;

DE 24-MAY-1996 (first entry)

KW Cedar pollen allergen A.

KW Cedar; pollen; allergen; immunoglobulin E; Ige; T-cell epitope;

KW antibody; pollinosis; therapy; immunotherapy.

OS Cryptomeria japonica.

PN EP-700929-A2.

PD 13-MAR-1996.

PE 08-SEP-1995; 306295.

PR 10-SEP-1994; JP-242137.

PR 14-JUL-1995; JP-200221.

PR 14-JUL-1995; JP-200204.

PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

PI Hino K, Saito S, Taniguchi Y;  
DR WPI: 96-140976/15.

PT New peptide(s) derived from cedar pollen allergens - activate

PT allergen-specific T-cells, but not allergen-specific Ige antibodies,

PS used for treating cedar pollinosis

Claim 5; Page 29-30; 36pp; English.

Synthetic peptides based on portions of cedar pollen allergens A

(R81586) and B (R81587) were tested for their ability to activate

CC cedar allergen-specific T-cells, but not allergen-specific Ige

CC antibodies. 6 peptides (R81580-R81585) were identified as T-cell

CC epitopes. These peptides, plus subsequences (R81573-79) essential

CC for T-cell recognition, and homologous peptides (R81588-96) can

be used as immunotherapeutic agents to treat or prevent cedar

CC pollinosis, avoiding side-effects such as anaphylaxis.  
Sequence 514 AA.

Query Match 22.7%; Score 129; DB 1; Length 514;  
Best Local Similarity 100.0%; Pred. No. 6,23e-03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 236 IDIFASKNFHLQKNTIGT 254  
IDIFASKNFHLQKNTIGT 49

RESULT 10  
ID W80357 standard; peptide: 47 AA.

AC W80357:  
DE 11-JAN-1999 (first entry)  
DE Sugi allergen protein Cryj1 derived epitope for T cells.  
KW T cell epitope; sugi allergen proteins Cryj1; Cryj2; treatment;  
KW sugi-pollinosis; allergic reaction; pollen.  
OS Synthetic.  
PN J10259198-A.  
PD 29-SEP-1998.  
PF 22-DEC-1997; 353448.  
PR 24-DEC-1996; JP-343441.  
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.  
PA (SANY) SANKYO CO LTD.  
DR WPI: 98-577037/49.  
PT A linked T cell epitope peptide - used for the treatment of  
PT sugi-pollinosis  
PS Claim 10; Page 5; 21pp; Japanese.  
CC W80339-58 represent epitopes for T cells, derived from the sugi allergen  
CC proteins Cryj1 (W80339-44, W80350-53 and W80356-58) and Cryj2 (W80345-49  
CC and W80354-55). The peptides are useful for the treatment of  
CC sugi-pollinosis, an allergic reaction of the body to pollen.  
SQ Sequence 47 AA;

Query Match 22.5%; Score 128; DB 1; Length 47;

Best Local Similarity 84.0%; Pred. No. 7,58e-03;  
Matches 21; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

Db 12 KLTSKTIASC-LNGIIAAYONPASM 35  
KLTSKTIASC-LNGIIAAYONPASM 79

RESULT 11  
ID W80347 standard; peptide: 17 AA.

AC W80347:  
DE 11-JAN-1999 (first entry)  
DE Sugi allergen protein Cryj2 derived epitope for T cells.  
KW T cell epitope; sugi allergen proteins Cryj1; Cryj2; treatment;  
KW sugi-pollinosis; allergic reaction; pollen.  
OS Synthetic.  
PN J10259198-A.  
PD 29-SEP-1998.  
PF 22-DEC-1997; 353448.  
PR 24-DEC-1996; JP-343441.  
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.  
PA (SANY) SANKYO CO LTD.  
DR WPI: 98-577037/49.  
PT A linked T cell epitope peptide - used for the treatment of  
PT sugi-pollinosis  
PS Claim 7; Page 18; 21pp; Japanese.  
CC W80339-58 represent epitopes for T cells, derived from the sugi allergen  
CC proteins Cryj1 (W80339-44, W80350-53 and W80356-58) and Cryj2 (W80345-49  
CC and W80354-55). The peptides are useful for the treatment of  
CC sugi-pollinosis, an allergic reaction of the body to pollen.  
SQ Sequence 17 AA;

Query Match 20.6%; Score 117; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6,45e-02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 IDIFASKNFHLQKNTIG 17  
IDIFASKNFHLQKNTIG 47

RESULT 12  
ID W80339 standard; peptide: 33 AA.

AC W80339:  
DE 11-JAN-1999 (first entry)  
DE Sugi allergen protein Cryj1 derived epitope for T cells.  
KW T cell epitope; sugi allergen proteins Cryj1; Cryj2; treatment;  
KW sugi-pollinosis; allergic reaction; pollen.  
OS Synthetic.  
PN J10259198-A.  
PD 29-SEP-1998.  
PF 22-DEC-1997; 353448.  
PR 24-DEC-1996; JP-343441.  
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.  
PA (SANY) SANKYO CO LTD.  
DR WPI: 98-577037/49.  
PT A linked T cell epitope peptide - used for the treatment of  
PT sugi-pollinosis  
PS Claim 10; Page 5; 21pp; Japanese.  
CC W80339-58 represent epitopes for T cells, derived from the sugi allergen  
CC proteins Cryj1 (W80339-44, W80350-53 and W80356-58) and Cryj2 (W80345-49  
CC and W80354-55). The peptides are useful for the treatment of  
CC sugi-pollinosis, an allergic reaction of the body to pollen.  
SQ Sequence 33 AA;

Query Match 20.6%; Score 117; DB 1; Length 33;

Best Local Similarity 67.7%; Pred. No. 6,45e-02;  
Matches 21; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

Db 1 FASKNFHLQKNTIGT-RRISLKLTSKTIASC 31  
FASKNFHLQKNTIGT-RRISLKLTSKTIASC 63

RESULT 13  
ID R81582 standard; peptide: 17 AA.

AC R81582:  
DE 24-MAY-1996 (first entry)  
DE Cedar pollen allergen peptide 10 (T-cell epitope).  
KW Cedar; Cryptomeria japonica; pollen; allergen; immunoglobulin E;  
KW IGE; T-cell epitope; antibody; pollinosis; therapy; immunotherapy.  
OS Synthetic.  
PN EP-700929-A2.  
PD 13-MAR-1996.  
PF 08-SEP-1995; 306295.  
PR 10-SEP-1994; JP-242137.  
PR 14-JUL-1995; JP-200221.  
PR 14-JUL-1995; JP-200204.  
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.  
PI Hino K. Saito S. Taniguchi Y;  
DR WPI: 96-140976/15.  
PT New peptide(s) derived from cedar pollen allergens - activate  
PT allergen-specific T-cells, but not allergen-specific IGE antibodies,  
PT used for treating cedar pollinosis  
PS Claim 4; Page 28; 36pp; English.  
CC Synthetic peptides based on portions of cedar pollen allergens A  
CC (R81586) and B (R81587) were tested for their ability to activate  
CC cedar allergen-specific T-cells, but not allergen-specific IGE  
CC antibodies. 6 peptides (R81580-R81585) were identified as T-cell  
CC epitopes. These peptides, plus subsequences (R81573-79) essential  
CC for T-cell recognition, and homologous peptides (R81588-96) can  
CC be used as immunotherapeutic agents to treat or prevent cedar  
CC pollinosis, avoiding side-effects such as anaphylaxis.  
SQ Sequence 17 AA;

Query Match 20.2%; Score 115; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9,47e-02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 DIFASKNFHLQKNTIGT 17  
OY 32 DIFASKNFHLQKNTIGT 48

DB 1 KVDGIITAYQNPASWK 16  
OY 65 RVDGIITAYQNPASWK 80

Search completed: Mon Jun 19 15:54:24 2000  
Job time : 9 secs.

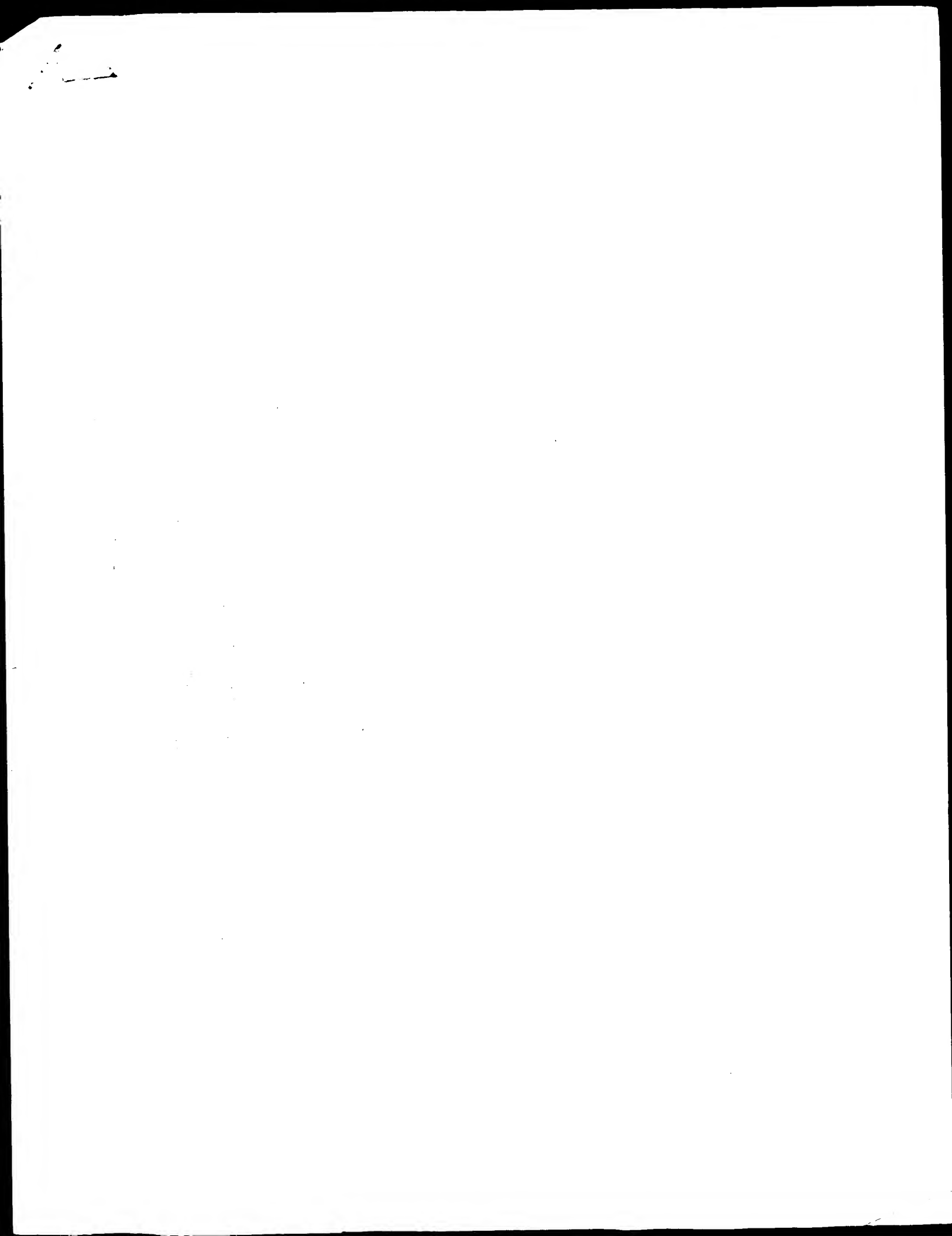
RESULT 14  
ID W80345 standard; peptide: 17 AA.  
AC W80345;  
DT 11-JAN-1999 (first entry)  
DE Sugi allergen protein Cryj2 derived epitope for T cells.  
KW T cell epitope; sugi allergen proteins Cryj1; Cryj2; treatment;  
OS sugi-pollinosis; allergic reaction; pollen.  
PN Synthetic  
PN J10259198.A.  
PD 29-SEP-1998.  
PE 22-DEC-1997; 353448.  
PR 24-DEC-1996; JP-343441.  
PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.  
PA (SANY ) SANKYO CO LTD.  
DR WPI: 98-577037/49.  
PT A linked T cell epitope peptide - used for the treatment of  
PT sugi-pollinosis  
PS Claim 7; Page 18; 21pp; Japanese.  
CC W80339-58 represent epitopes for T cells, derived from the sugi allergen  
CC proteins Cryj1 (W80339-44, W80350-53 and W80356-58) and Cryj2 (W80345-49  
CC and W80354-55). The peptides are useful for the treatment of  
CC sugi-pollinosis, an allergic reaction of the body to pollen.  
SQ Sequence 17 AA;

Query Match 19.5%; Score 111; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 2.03e-01;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DB 1 KVDGIITAYQNPASWK 16  
OY 65 RVDGIITAYQNPASWK 80

RESULT 15  
ID R81580 standard; Peptide; 17 AA.  
AC R81580;  
DT 24-MAY-1996 (first entry)  
DE Cedar pollen allergen peptide 8 (T-cell epitope).  
KW Cedar; Cryptomeria japonica; pollen; allergen; immunoglobulin E;  
KW IGE; T-cell epitope; antibody; pollinosis; therapy; immunotherapy.  
OS Synthetic  
PN EP-700929-A2.  
PD 13-MAR-1996.  
PE 08-SEP-1995; 306295.  
PR 10-SEP-1994; JP-242137.  
PR 14-JUL-1995; JP-200221.  
PR 14-JUL-1995; JP-200204.  
PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.  
PI Hino K, Saito S, Taniguchi Y;  
DR WPI: 96-140976/15.  
PT New peptide(s) derived from cedar pollen allergens - activate  
PT allergen-specific T-cells, but not allergen-specific IGE antibodies,  
PT used for treating cedar pollinosis  
PS Claim 4; Page 28; 36pp; English.  
CC Synthetic peptides based on portions of cedar pollen allergens A  
CC (R81586) and B (R81587) were tested for their ability to activate  
CC cedar allergen-specific T-cells; but not allergen-specific IGE  
CC antibodies. 6 Peptides (R81580-R81585) were identified as T-cell  
CC epitopes. These peptides, plus subsequences (R81573-79) essential  
CC for T-cell recognition, and homologous peptides (R81588-96) can  
CC be used as immunotherapeutic agents to treat or prevent cedar  
CC pollinosis, avoiding side-effects such as anaphylaxis.  
SQ Sequence 17 AA;

Query Match 19.5%; Score 111; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 2.03e-01;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;



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Run on: Mon Jun 19 15:53:44 2000; MasPar time 9.04 seconds

417.392 million cell updates/sec

>US-09-142-524A-1

Description:	(1-80) from US09142524A.pep
Perfect Score:	569
Sequence:	1 MKVTVAENQFGPNRRVETKP

### Scoring table:

searched: 142080 seqs, 47172406 residues

✓ Existing first 45 summaries

Database:

Statistics: Mean 39.829; Variance 80.867; scale 0.493

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

Result No.	Query Score	Match	Length	DB	ID	Description
---------------	----------------	-------	--------	----	----	-------------

	Pred. No.	Description
1	129	second major allergen Cry j II protein - Ja
2	128	DNA topoisomerase I -
3	98	FHM2 protein - yeast
4	97	hypothetical nucleic acid-binding protein
5	96	major allergen Cry j
6	95	adhesion-type protein
7	94	Kallmann syndrome pro
8	93	ATP-binding transport
9	92	hypothetical protein
10	91	riboflavin synthase,
11	90	glyceralddehyde-3-phos
12	89	sensory transduction
13	88	subtilisin-like prote
14	87	probable membrane pro
15	86	hypothetical protein
16	85	hypothetical protein
17	84	hypothetical protein
18	83	hypothetical protein
19	82	hypothetical protein
20	81	hypothetical protein
21	80	hypothetical protein
22	79	Cot intron A protein
23	78	hypothetical protein

24	84	14.8	336	2	S71350	glyceralddehyde-3-phos	8.64e+00
25	84	14.8	1330	2	B70836	hypothetical protein	8.64e+00
26	84	14.8	3229	2	S78782	probable cell-surface	8.64e+00
27	83	14.6	243	2	D75146	ssu ribosomal protein	1.14e+01
28	83	14.6	773	2	T00554	hypothetical protein	1.14e+01
29	83	14.6	1205	2	A35547	Ca2+-transporting ATP	1.14e+01
30	83	14.6	1745	2	S44816	Nucleotide-binding pr	1.14e+01
31	82	14.4	249	2	D64310	band-6-protein - bovi	1.50e+01
32	82	14.4	295	2	S60711	band-6-protein - bovi	1.50e+01
33	82	14.4	336	2	A42963	glyceraldhyde-3-phos	1.50e+01
34	82	14.4	389	2	S73910	probable serine/chiro	1.50e+01
35	82	14.4	497	2	B71677	histidine kinase sens	1.50e+01
36	81	14.2	725	2	S60712	band-6-protein - huma	1.50e+01
37	81	14.2	402	2	I67760	transposase - Escheri	1.98e+01
38	81	14.2	454	2	G71703	hypothetical protein	1.98e+01
39	81	14.2	707	2	T00665	xanthine dehydrogen	1.98e+01
40	81	14.2	729	2	S73093	hypothetical protein	1.98e+01
41	81	14.2	982	2	T15667	hypothetical protein	1.98e+01
42	81	14.2	1011	2	S65668	preprotein translocas	1.98e+01
43	81	14.2	1116	2	T14598	polyprotein - slime m	1.98e+01
44	80	14.1	1225	2	T08467	aspartate racemase (E	2.59e+01
45	80	14.1	351	2	F72552	hypothetical protein	2.59e+01

## RESULT 1

ENTRY	#type complete
JC2498	second major allergen Cry j II precursor - Japanese cedar
TITLE	#formal_name Cryptomeria japonica #common_name Japanese cedar
ORGANISM	16-Mar-1995 #sequence_revision 26-May-1995 #text_change
DATE	12-Sep-1997

## REFERENCE

#journal

井上

##mq1

##CLO;

###mol

## REFERENCE

# Journal

1  
2  
3  
4  
5  
6

#access1c

## ##res1

FEATURE  
1-5A

○  
○  
●  
○  
○

.....

Best Local  
Matchbox

236 TD

31 ID







Query Match 16.7%; Score 95; DB 2; Length 374;  
 Best Local Similarity 100.0%; Pred. No. 3.50e-01;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 234 MKVYAFNQGPN 246  
 1 MKVYAFNQGPN 13

RESULT 8  
 ENTRY A40351 #type complete  
 TITLE adhesion-type protein ADMLX - human  
 ORGANISM #formal\_name Homo sapiens #common\_name man  
 DATE 24-Jan-1992 #sequence\_revision 24-Jan-1992 #text\_change 20-Mar-1998

ACCESSIONS A40351  
 REFERENCE A40351  
 #authors Legouis, R.; Hardelin, J.P.; Levilliers, J.; Clavier, J.M.; Compain, S.; Wunderle, V.; Millaudeau, P.; Le Paslier, D.; Cohen, D.; Caterina, D.; Bouquelier, L.; Delamarre-Van de Maal, H.; Lutfalla, G.; Weissenbach, J.; Petit, C.

#journal Cell (1991) 67:423-435  
 #title The candidate gene for the X-linked Kallmann syndrome encodes a protein related to adhesion molecules.  
 #cross-references M0ID:92005720  
 #accession A40351

GENETICS #status preliminary  
 #molecule-type mRNA  
 #residues 1-679 ##label LEG  
 #cross-references GB:S60085; NID:g237595; PID:g237597

FEATURES #gene GDB:KAL1, KAL  
 #cross-references GDB:120116; OMIM:308700  
 #map\_position Xp22.32-Xp22.32  
 CLASSIFICATION #superfamily antileukoprotease repeat homology  
 FEATURE 129-175 #domain antileukoprotease repeat homology #label ALP  
 SUMMARY #length 679 #molecular-weight 76301 #checksum 1231

Query Match 16.7%; Score 95; DB 2; Length 679;  
 Best Local Similarity 27.1%; Pred. No. 3.50e-01;  
 Matches 16; Conservative 19; Mismatches 23; Indels 1; Gaps 1;

Db 247 VQLTDIRPQW-YQFRVAANVHGRTAPSKHFRSSKDPSPAPANRLANSTVNS 304  
 5 VAFNQGPNRRVFKRVSNIHGRIDIFASKNPHLQKNTIGTRISLKLISGKIAS 63

RESULT 9  
 ENTRY S17982 #type complete  
 TITLE Kallmann syndrome protein KALIG-1 - human  
 ORGANISM #formal\_name Homo sapiens #common\_name man  
 DATE 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 19-Feb-1999

ACCESSIONS S17982  
 REFERENCE S17982  
 #authors Franco, B.; Guioili, S.; Pragliola, A.; Incerti, B.; Bargon, B.; Tonlorenzi, R.; Carozzo, R.; Maestri, E.; Pieretti, M.; Tallon-Miller, P.; Brown, C.J.; Willard, H.F.; Lawrence, C.; Persico, M.G.; Camerino, G.; Ballabio, A.  
 #journal Nature (1991) 353:529-536  
 #title A gene deleted in Kallmann's syndrome shares homology with neural cell adhesion and axonal path-finding molecules.  
 #cross-references M0ID:92018217  
 #accession S17982

GENETICS #status preliminary  
 #molecule-type mRNA  
 #residues 1-680 ##label FRA  
 #cross-references EMBL:X60299; NID:g34024; PID:g34025  
 #gene GDB:KAL1, KAL  
 #cross-references GDB:120116; OMIM:308700  
 #map\_position Xp22.32-Xp22.32

CLASSIFICATION #superfamily antileukoprotease repeat homology  
 FEATURE 130-176 #domain antileukoprotease repeat homology #label ALP  
 SUMMARY #length 680 #molecular-weight 76151 #checksum 5161

Query Match 16.7%; Score 95; DB 2; Length 680;  
 Best Local Similarity 27.1%; Pred. No. 3.50e-01;  
 Matches 16; Conservative 19; Mismatches 23; Indels 1; Gaps 1;

Db 248 VQLTDIRPQW-YQFRVAANVHGRTAPSKHFRSSKDPSPAPANRLANSTVNS 305  
 5 VAFNQGPNRRVFKRVSNIHGRIDIFASKNPHLQKNTIGTRISLKLISGKIAS 63

RESULT 10  
 ENTRY S55415 #type complete  
 TITLE ABC transporter (ATP-binding protein) ywja  
 ORGANISM #formal\_name Bacillus subtilis  
 DATE 15-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 20-Sep-1999

ACCESSIONS S55415  
 REFERENCE S55415  
 #authors Glaser, P.; Danchin, A.  
 #description submitted to the EMBL Data Library, May 1995  
 #submision Cloning and sequencing of the Bacillus subtilis chromosomal region from 320 degrees to 321 degrees.  
 #accession S55415

GENETICS #molecule-type DNA  
 #residues 1-575 ##label GTA  
 #cross-references EMBL:249782; NID:9853752; PIDN:CAA9862.1; PID:9853754

REFERENCE A69580  
 #authors Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bortero, M.G.; Bessieres, P.; Bolotin, A.; Borchert, S.; Bortis, R.; Boutsier, L.; Brans, A.; Braun, M.; Brignell, S.C.; Bron, S.; Brouillet, S.; Brunsch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi, S.K.; Codani, U.J.; Conerton, I.F.; Cummings, N.J.; Daniel, R.A.; Denzot, F.; Devigne, K.M.; Duesterhoeft, A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.; Foulger, D.; Fitz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallier, N.; Ghim, S.Y.; Glaser, P.; Goffeau, A.; Gollightly, E.J.; Grand, G.; Giuseppe, G.; Guy, B.J.; Hage, K.; Haleb, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Itaya, M.; Jones, L.; Joris, B.; Karamata, D.; Kasahara, Y.; Klaerr-Blanchard, M.; Klein, C.; Kobayashi, Y.; Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, S.; Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, C.; Medigue, C.; Medina, N.; Mellado, R.P.; Mizuno, M.; Moesli, D.; Nakai, S.; Noback, M.; Noone, D.; O'Reilly, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetlelle, D.; Potwolk, S.; Prescott, A.M.; Prescan, E.; Puje, P.; Purnelle, B.; Rapoport, G.; Rey, M.; Reynolds, S.; Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadleir, Y.; Sato, T.; Scanlon, E.; Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serio, S.J.; Serro, P.; Shin, B.S.; Soldo, B.; Sorokin, A.; Tacconi, E.; Takagi, T.; Takahashi, H.; Takemura, K.; Takeuchi, M.; Tamakoshi, A.; Tanaka, S.; Terpestra, P.; Tognoni, A.; Tosato, V.; Uchiyama, S.; Vandenbol, M.; Vannier, F.; Vassarotti, A.; Viari, A.; Wandurt, R.; Wedler, E.; Wedler, H.; Weitznegger, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasunoto, K.; Yata, K.; Yoshida, K.; Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.

#journal Nature (1997) 390:249-256  
 #title The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
 #cross-references M0ID:98044033  
 #accession G70059

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##status      nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues    1-575 #label K0N
##cross-references GB:299123; GB:AL009126; NID:q2636240;
##experimental_source strain 168
GENETICS
#gene         ywja
#start_codon  GTG
#classification #superfamily unassigned ATP-binding cassette proteins;
#feature      ATP-binding cassette homology
KEYWORDS
349-543
366-373
SUMMARY
#domain ATP-binding cassette homology #label ABC\
#region nucleotide-binding motif A (P-loop)
#length 575 #molecular_weight 64562 #checksum 4403
Query Match 16.5%; Score 94; DB 2; Length 575;
Best Local Similarity 29.2%; Pred. No. 4,73e-01;
Matches 19; Conservative 17; Mismatches 27; Indels 2; Gaps 2;
Db 176 KMTKATFTINKDIGDFSAVENNIGIRLQAFNGAEFEKRPVANNQFRVT-KLSSY 234
QY 1 MKYVAENQGFPMNRVRIKRVSNVHIGRIDIFASKNFHLQKNTIGTGR-RISLKLTSG 59
Db 235 KIMAK 239
QY 60 KIASR 64

RESULT 11
ENTRY 11
TITLE T15183 #type complete
ORGANISM hypothetical protein C18E3.3 - Caenorhabditis elegans
DATE 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change
ACCESSIONS
REFERENCE T15183
#authors Connell, M.; Magg, L.
#description Submitted to the EMBL Data Library, April 1997
#accession T15183
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-893 #label CON
#cross-references EMBL:AF000265; NID:q1947147; PID:q1947148;
#experimental_source strain Bristol N2; clone C18E3
GENETICS
#gene CESP:C18E3.3
#map_position 1
#introns 25/3; 66/2; 108/3; 142/1; 185/2; 380/1; 597/1; 744/2; 792/3
#length 893 #molecular_weight 102424 #checksum 6553
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Best Local Similarity 31.3%; Pred. No. 4,73e-01;
Matches 20; Conservative 20; Mismatches 20; Indels 4; Gaps 4;
Db 602 VSLKATNVPEAP-FTYSTRKNQLEHSTPEYPARISIQFEPKLISNOKPD-IFKQY 659
QY 16 VFIRKSVNIIHGRIDIFASKN-F-HLQKNTIGTGRISLKLTSKIASRVDGIIAAAY 73
Db 660 HLPT 663
QY 74 ONPA 77

RESULT 12
ENTRY 12
TITLE F72207 #type complete
ORGANISM riboflavin synthase, alpha subunit - Thermotoga maritima
#formal_name Thermotoga maritima
DATE 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change

```

```

ACCESSIONS
REFERENCE F72207
#authors Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson,
R.U.; Haft, D.H.; Hickey, E.K.; Peterson, J.D.; Nelson,
W.C.; Ketchum, K.A.; McDonald, L.; Utterback, T.R.; Malek,
J.A.; Linber, K.D.; Garrett, M.M.; Stewart, A.M.; Cotton,
M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
Heidelberg, J.; Sutton, G.G.; Fleischmann, R.D.; White, O.;
Salzberg, S.L.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Nature (1999) 399:323-329
Evidence for lateral gene transfer between Archaea and
Bacteria from genome sequence of Thermotoga maritima.
#journal Nature
#title Evidence for lateral gene transfer between Archaea and
#cross-references MUID:99287316
#accession F72207
#status preliminary
#molecule_type DNA
#residues 1-190 #label ARN
#cross-references GB:AE001819; GB:AE000512; NID:q4982396; PID:q4982409;
#experimental_source strain MSB8
GENETICS
#gene TM1827
#classification #superfamily riboflavin synthase alpha chain
#accession TM1827
#length 190 #molecular_weight 21678 #checksum 6856
Query Match 15.6%; Score 89; DB 2; Length 190;
Best Local Similarity 28.6%; Pred. No. 2.08e+00;
Matches 10; Conservative 13; Mismatches 11; Indels 1; Gaps 1;
Db 60 RRTNFVSRFYNLEK-SLAGSRVEGLVYGHWDG 93
QY 29 RRIIDFASKNFHLQKNTIGTGRISLKLTSKIAS 63

RESULT 13
ENTRY 13
TITLE G69628 #type complete
ORGANISM glyceroldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) gaps -
DATE 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change
ACCESSIONS
REFERENCE G69628
#authors Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.;
Alloni, G.; Azevedo, V.; Bartero, M.G.; Bessieres, P.;
Biolotin, A.; Borchert, S.; Boriss, R.; Boursier, L.; Brans,
A.; Braun, M.; Brignell, S.C.; Bron, S.; Brouillet, S.;
Brusch, C.V.; Caldwell, B.; Capiano, V.; Carter, N.M.;
Choi, S.K.; Codani, J.J.; Conerton, I.F.; Cummings, N.J.;
Daniel, R.A.; Denizot, F.; Devigne, K.M.; Duesterhoeft, A.;
Ehrlich, S.D.; Emerson, P.T.; Ehtani, K.D.; Erlington, J.;
Fabret, C.; Ferrari, E.; Fougere, D.; Fritz, C.; Fujita,
M.; Fujita, Y.; Fuma, S.; Gallizi, A.; Gallier, N.; Ghim,
S.Y.; Glaeser, P.; Goffeau, A.; Golightly, E.J.; Grand, G.;
Gusteppi, G.; Guy, B.J.; Haga, K.; Haeche, J.; Harwood,
C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.;
Hullo, M.F.; Itaya, M.; Jones, L.; Joris, B.; Karamata, D.;
Kasahara, Y.; Klaier-Bianchini, M.; Klein, C.; Kobayashi,
Y.; Koetler, P.; Koningsstein, G.; Krogh, S.; Kumano, M.;
Kunita, K.; Lapidus, A.; Lardinois, S.; Lauber, J.;
Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.;
Maueel, C.; Medigue, C.; Medina, N.; Melado, R.P.; Mizuno,
M.; Moestl, D.; Nakai, S.; Nodack, M.; Noone, D.; O'Reilly,
M.; Ogawa, K.; Ogihara, A.; Oudega, B.; Park, S.H.; Parro,
V.; Pohl, T.M.; Portelle, D.; Portelle, B.; Rapoport, G.;
Rey, M.; Reynolds, S.; Rieger, M.; Rivolta, C.; Rocha, E.;
Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon, E.;
Sekowska, A.; Seror, S.J.; Serrero, P.; Shin, B.S.; Soldo,
B.; Sorokin, A.; Tacconi, E.; Takagi, T.; Takahashi, H.;
Takemaru, K.; Takeuchi, M.; Tamakoshi, A.; Tanaka, T.;

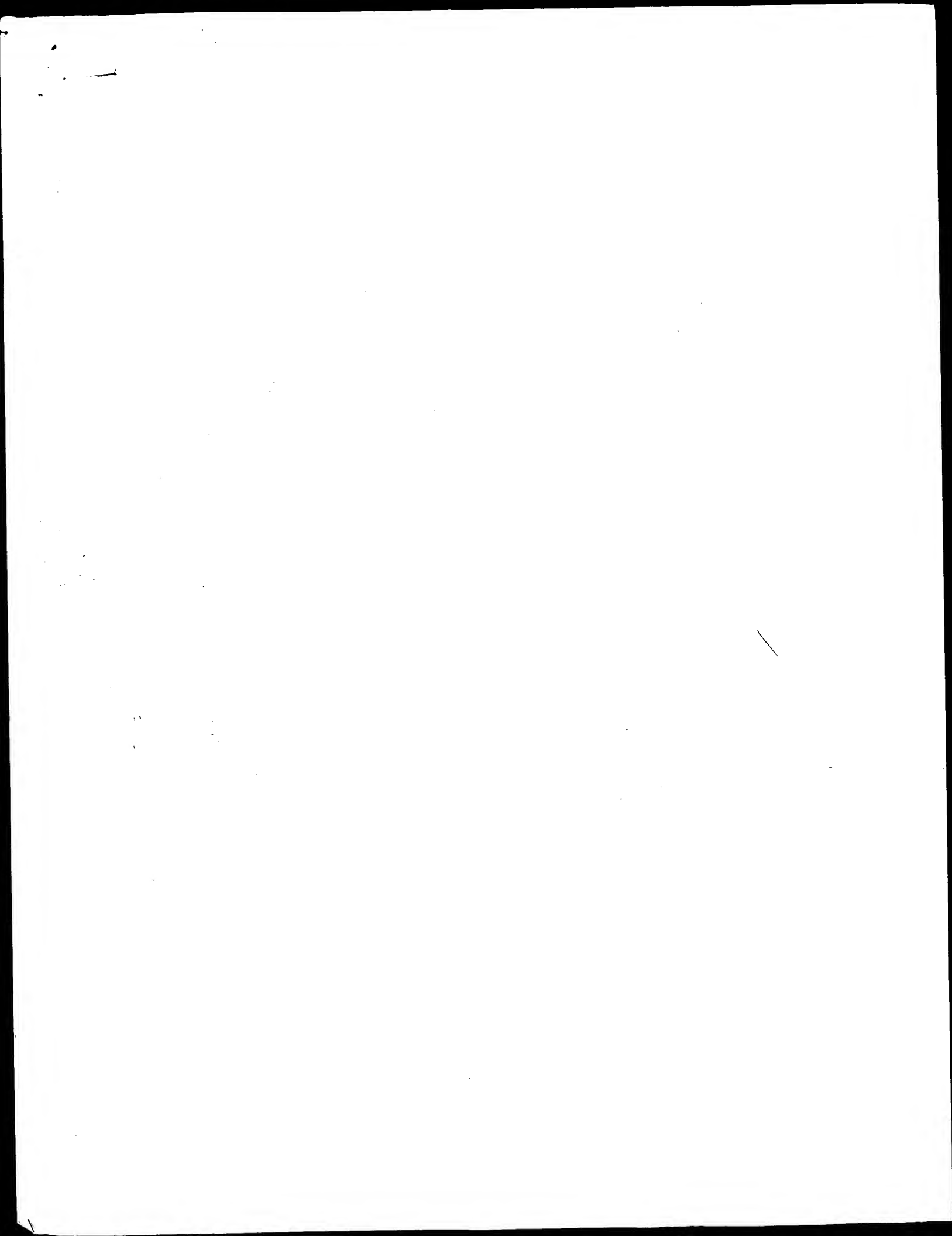
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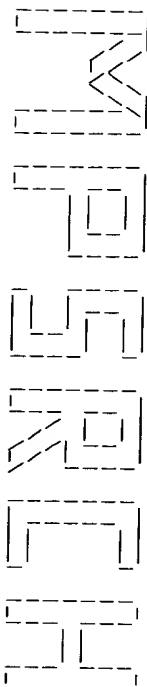


Wed Jun 21 09:22:48 2000

Job time : 14 secs.

US-09-142-524A-1.rpt





(TM)

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MPsrch.mp protein - protein database search, using Smith-Waterman algorithm  
Run on: Mon Jun 19 15:52:40 2000; Maspar time 5.85 seconds  
Tabular output not generated. 416,406 Million cell updates/sec

Title: >US-09-142-524A-1  
Description: (1-80) from US09142524A.pep  
Perfect Score: 569  
Sequence: 1 MKYTVAFNCRGPNRRVFIRK.....IASRRVDGIATAYQNPASWK 80

Scoring table:  
PAM 150  
Gap 11

Searched: 83857 seqs, 30454973 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: swiss-prot38  
1:swissprot

Statistics: Mean 40.706; Variance 73.263; scale 0.556

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	129	22.7	514	1	MPA2_CRYTA POSSIBLE POLYGALACTURO	3.32e-07
2	98	17.2	633	1	TOP1_THEMA DNA TOPOISOMERASE I (E	3.02e-02
3	97	17.0	862	1	FKH2_YEAST FORK HEAD PROTEIN HOMO	4.25e-02
4	96	16.9	507	1	DNA_RHIME CHROMOSOMAL REPLICATIO	5.96e-02
5	95	16.7	110	1	Y12K_SMSV4 POSSIBLE 12 KD NUCLEIC	8.34e-02
6	95	16.7	374	1	SBP_CRYTA SUCI BASIC PROTEIN PRE	8.34e-02
7	95	16.7	680	1	KALM_HUMAN KALIMANN SYNDROME PROT	8.34e-02
8	94	16.5	575	1	YWJA_BACSU HYDROLYTICAL ABC TRANS	1.16e-01
9	89	15.6	340	1	G3P2_BACSU GLYCERALDEHYDE 3-PROSP	5.96e-01
10	87	15.3	478	1	YSP3_YEAST SUBTILISIN-LIKE PROTEA	1.13e+00
11	86	15.3	629	1	FRE7_YEAST FERRIC REDUCTASE TRANS	1.13e+00
12	86	15.1	532	1	PECK_AMASU PHOSPHOENOLPYRUVATE CA	1.54e+00
13	86	15.1	1070	1	YQFA_YEAST HYDROLYTICAL 123.0 KD	1.54e+00
14	85	14.9	331	1	YQF1_YEAST HYDROLYTICAL 35.6 KD P	2.10e+00
15	85	14.9	394	1	DNA_YEAST CHROMOSOMAL REPLICATIO	2.10e+00
16	84	14.8	263	1	DNA_SPTAP CHROMOSOMAL REPLICATIO	2.86e+00
17	83	14.6	302	1	HYPR_BACSU HYDROLYTICAL 44.4 KD P	3.89e+00
18	83	14.6	1205	1	ATCR_HUMAN CALCIN-TRANSPORTING A	3.89e+00
19	83	14.6	1745	1	YLS1_CAREL HYDROLYTICAL 113.2 KD	1.28e+01
20	82	14.4	249	1	Y084_METJA HYPOHETICAL AMP-BINDI	5.27e+00
21	82	14.4	389	1	PKNS_MYCPN PUTATIVE SERINE/THREON	5.27e+00
22	81	14.2	1011	1	SECA_PEA PREPROTEIN TRANSLOCASE	7.11e+00
23	80	14.1	155	1	RS7_MYCGE 305 RIBOSOMAL PROTEIN	9.57e+00

24	80	14.1	159	1	RK35_SPTOL 50S RIBOSOMAL PROTEIN	9.57e+00
25	80	14.1	274	1	Y179_MYCGE HYDROLYTICAL ABC TRANS	9.57e+00
26	80	14.1	311	1	NFE2_RHIME NFE2 PROTEIN	9.57e+00
27	80	14.1	317	1	YV91_YEAST METL_YEAST S-ADENOSYLMETHIONINE S	9.57e+00
28	80	14.1	383	1	YV01_YEAST METL_YEAST S-ADENOSYLMETHIONINE S	9.57e+00
29	80	14.1	419	1	YV01_YEAST METL_YEAST S-ADENOSYLMETHIONINE S	9.57e+00
30	80	14.1	421	1	YV01_YEAST METL_YEAST S-ADENOSYLMETHIONINE S	9.57e+00
31	80	14.1	472	1	YV01_YEAST METL_YEAST S-ADENOSYLMETHIONINE S	9.57e+00
32	80	14.1	493	1	YV01_YEAST METL_YEAST S-ADENOSYLMETHIONINE S	9.57e+00
33	80	14.1	719	1	YV01_YEAST METL_YEAST S-ADENOSYLMETHIONINE S	9.57e+00
34	79	13.9	177	1	YV01_YEAST METL_YEAST S-ADENOSYLMETHIONINE S	9.57e+00
35	79	13.9	243	1	YV01_YEAST METL_YEAST S-ADENOSYLMETHIONINE S	9.57e+00
36	79	13.9	325	1	YV01_YEAST METL_YEAST S-ADENOSYLMETHIONINE S	9.57e+00
37	79	13.9	325	1	YV01_YEAST METL_YEAST S-ADENOSYLMETHIONINE S	9.57e+00
38	79	13.9	436	1	YV01_YEAST METL_YEAST S-ADENOSYLMETHIONINE S	9.57e+00
39	79	13.9	519	1	YV01_YEAST METL_YEAST S-ADENOSYLMETHIONINE S	9.57e+00
40	79	13.9	719	1	YV01_YEAST METL_YEAST S-ADENOSYLMETHIONINE S	9.57e+00
41	79	13.9	1010	1	YV01_YEAST METL_YEAST S-ADENOSYLMETHIONINE S	9.57e+00
42	79	13.9	1103	1	YV01_YEAST METL_YEAST S-ADENOSYLMETHIONINE S	9.57e+00
43	78	13.7	176	1	YV01_YEAST METL_YEAST S-ADENOSYLMETHIONINE S	9.57e+00
44	78	13.7	473	1	YV01_YEAST METL_YEAST S-ADENOSYLMETHIONINE S	9.57e+00
45	78	13.7	577	1	YV01_YEAST METL_YEAST S-ADENOSYLMETHIONINE S	9.57e+00

## ALIGNMENTS

RESULT	ID	MPA2_CRYTA	STANDARD	PRT	514 AA.
AC	P43212				
DT	01-NOV-1995 (Rel. 32, Created)				
DT	01-NOV-1995 (Rel. 32, Last sequence update)				
DT	01-NOV-1997 (Rel. 35, Last annotation update)				
DE	POSSIBLE POLYGALACTURONASE PRECURSOR (EC 3.2.1.15) (PG) (PECTINASE)				
DE	(MAJOR POLLEN ALLERGEN CRT j 2) (CRY j II).				
OS	Cryptomeria japonica (Japanese cedar).				
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;				
OC	euphyllophytes; Spermatophyta; Coniferopsida; Coniferales;				
OC	Taxodiaceae; Cryptomeria.				
RN	[1]				
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.				
RC	TISSUE-POLLEN;				
RC	MEDLINE: 95010777.				
RA	Namda M., Kurose M., Torioge K., Hino K., Taniguchi Y., Fukuda S.,				
RA	Usui M., Kurimoto M.,				
RT	"Molecular cloning of the second major allergen, Cry j II, from				
RT	Japanese cedar pollen.";				
RL	FEBS Lett. 353:124-128(1994).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE-POLLEN;				
RC	MEDLINE: 94271186.				
RA	Komiyama N., Sone T., Shimizu K., Morikubo K., Kino K.,				
RA	"cDNA cloning and expression of Cry j II the second major allergen of				
RT	Japanese cedar pollen.";				
RL	Biochem. Biophys. Res. Commun. 201:1021-1028(1994).				
RN	[3]				
RP	SEQUENCE OF 55-64.				
RC	MEDLINE: 90342988.				
RA	Sakaguchi M., Inouye S., Tanai M., Ando S., Usui M., Matunasi T.,				
RT	"Identification of the second major allergen of Japanese cedar				
RL	pollen.";				
CC	Allergy 45:309-312(1990).				
CC	-1- CATALYTIC ACTIVITY: RANDOM HYDROLYSIS OF 1,4-ALPHA-D-				
CC	-1- GALACTOSIDURONIC LINKAGES IN PECTANE AND OTHER GALACTURONANS.				
CC	-1- SUBCELLULAR LOCATION: SECRETED OR AMYLOPLAST (POTENTIAL).				
CC	-1- SIMILARITY: BELONGS TO FAMILY 28 OF GLYCOSYL HYDROLASES				
CC	(POLYGALACTURONASES).				
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CC EMBL: D37765; BAA07021.1; -

DR EMBL: D29772; BAA06172.1; -

DR PROSITE: PS00502; POLYGALACTURONASE; 1.

DR PFM: PFO0295; Glyco\_hydro.28; 1.

KM Hydrolase: Glycosidase; Cell wall; signal; zymogen; Fruit ripening;

KM Amyloplast; Glycoprotein; Allergen.

FT SIGNAL 1 2

FT PROPEP 45

FT CHAIN 46 433

FT PROPEP 434 514

FT ACT\_SITE 278 278

FT CARBOHYD 460 460

FT CARBOHYD 472 472

FT CONFLICT 5 5

FT CONFLICT 12 12

FT CONFLICT 34 35

FT CONFLICT 37 37

FT CONFLICT 88 88

FT CONFLICT 98 98

FT CONFLICT 451 451

FT CONFLICT 454 454

FT CONFLICT 504 504

FT CONFLICT 507 507

SEQUENCE 514 AA; 56645 MW; 624611C3FAD6302 CRC64;

Query Match 22.7%; Score 129; DB 1; Length 514;

Best Local Similarity 100.0%; Pred. No. 3,32e-07;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 236 IDIFASKNFHLQKNTIGTG 254

OY 31 IDIFASKNFHLQKNTIGTG 49

RESULT 2 STANDARD: PRT: 633 AA.

ID TOP1\_THEME

AC P46799; 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 15-FEB-2000 (Rel. 39, Last annotation update)

DE DNA TOPOISOMERASE I (EC 5.99.1.2) (OMEGA-PROTEIN) (RELAXING ENZYME)

DE (UNWISTING ENZYME) (SMILELASE).

GN TOPA OR TM0258.

OS Thermotoga maritima.

OC Bacteria; Thermotogales; Thermotoga.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-MSB8 / DSM 3109;

RX MEDLINE: 96136548.

RA Bouthier de la Tour C., Kaltoun H., Portemer C., Confalonieri F.,

RA Huber R., Duguet M.;

RT "Cloning and sequencing of the gene coding for topoisomerase I from

RT the extremely thermophilic eubacterium, Thermotoga maritima.";

RL Biochim. Biophys. Acta 1264:279-283(1995).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-MSB8 / DSM 3109;

RX MEDLINE: 99287316.

RA Nelson K.E., Clayton R.A., Gill S.R., Gwin M.L., Dodson R.J.,

RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,

RA McDonald L., Utterback T.R., Pratt M.S., Phillips C.A., Richard D.,

RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richard D.,

RA Salberg S.L., Smith H.O., Venter J.C., Fraser C.M.;

RT "Evidence for lateral gene transfer between Archaea and Bacteria from

RT genome sequence of Thermotoga maritima.";

RL Nature 399:323-329(1999).

CC -1- FUNCTION: THE REACTION CATALYZED BY TOPOISOMERASES LEADS TO THE

CC -1- CONVERSION OF ONE TOPOLOGICAL ISOMER OF DNA TO ANOTHER.

CC -1- CATALYTIC ACTIVITY: ATP-INDEPENDENT BREAKAGE OF SINGLE-STRANDED

CC FOLLOWED BY PASSAGE AND REJOINING.

CC -1- SUBUNIT: MONOMER (BY SIMILARITY).

CC -1- MISCELLANEOUS: WHEN A TOPOISOMERASE TRANSIENTLY BREAKS A DNA

CC BACKBONE BOND, IT SIMULTANEOUSLY FORMS A PROTEIN-DNA LINK, IN

CC WHICH A TYROSYL OXYGEN IN THE ENZYME IS JOINED TO A DNA PHOSPHORUS

CC AT ONE END OF THE ENZYME-SEVERED DNA STRAND.

CC -1- SIMILARITY: BELONGS TO PROKARYOTIC TYPE I/III TOPOISOMERASE

CC FAMILY.

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CC EMBL: U27841; AAA68949.1; -

DR EMBL: AE001708; AAD35346.1; -

DR TIGR: TM0258; -

DR HSSP: P06612; IECI.

DR PRINTS: PR00417; PRPISMRASEI.

DR PROSITE: PS00396; TOPOISOMERASE\_L\_PROK; 1.

DR PFM: PFO1131; Topoisom\_dac; 1.

KW Isomerase; Topoisomerase; DNA-binding.

FT ACT\_SITE 288 288

FT ACT\_SITE 288 288

SEQUENCE 633 AA; 72694 MW; F7262A044060CFE9 CRC64;

Query Match 17.2%; Score 98; DB 1; Length 633;

Best Local Similarity 26.6%; Pred. No. 3.02e-07;

Matches 17; Conservative 18; Mismatches 26; Indels 3; Gaps 3;

DB 96 IARVNTLGRKRI-VFSEITPRVREAVKKNPREIDMKKVAQOLA-RRIDRIYISLSP 153

OY 18 ITRVSVIIRHGRIDIFASKNFHLQKNTIGGRISLKLTSGLIASRRVDGIATAYO-NP 76

DB 154 VLNR 157

OY 77 ASWK 80

RESULT 3 STANDARD: PRT: 862 AA.

ID FKX2\_YEAST

AC P41813; 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE FORK HEAD PROTEIN HOMOLOG 2.

GN FKX2 OR YNL068C OR NZ403 OR YNL2403C.

GN Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;

OC Saccharomycetaceae; Saccharomyces.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-S288C;

RX Zhu G., Davis T.N.;

RT Submitted (Xxx-1995) to the EMBL/Genbank/DBJ databases.

RL [2]

RP SEQUENCE FROM N.A.

RC STRAIN-S288C / FY1679;

RX MEDLINE: 96267764.

RA Boehlmann R., Phillipsen P.;

RT "Sequencing a cosmid clone of Saccharomyces cerevisiae chromosome XIV

RT reveals 12 new open reading frames (ORFs) and an ancient duplication

RT of six ORFs.";

RL Yeast 12:391-402(1996).

RN [3]

RP SEQUENCE OF 1-440 FROM N.A.

RC STRAIN-S288C / FY1676;

RX MEDLINE: 96021608.

RA Berge P., Dolignon F., Crouzet M.;

RT "The sequence of a 44 420 bp fragment located on the left arm of

RT chromosome XIV from Saccharomyces cerevisiae.";



```
CC      -1- SIMILARITY: BELONGS TO THE DNA FAMILY.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; L25439; AAA26258.1; -.
DR      EMBL; L39265; AAA91097.1; -.
DR      PRINTS; PRO00051; DNAA.
DR      PROSITE; PS01008; DNAA, 1.
KM      PRAM; PF00308; bac_dnaa; 1.
KW      DNA replication; DNA-binding; ATP-binding.
FT      NP_BIND        208      215      ATP (PROBABLE).
SQ      SEQUENCE       507 AA; 56531 MW; 76015F49184F3CFA CRC64;

Query Match          16.7%; Score 96; DB 1; Length 507;
Best Local Similarity 24.3%; Pred. No. 5,96e-02;
Matches 17; Conservative 25; Mismatches 25; Indels 3; Gaps 3;

Db      422 VYAKHYNSRQELVSNRRTRIVKPRQJAMYLSKITLT-PSRFPEIGRGFGROHTYLHA 480
OY      5 VAFNQGPPNRVFEI-KRVSNVIITHGRIDIFASKNFHLQNKTIIGRRISLK-LTSKIA 62
Db      481 VKRIEELISA 490
OY      63 SRKVDTITAA 72

RESULT 5
ID      Y12K_SMSV4 STANDARD; PRT; 110 AA.
DC      P36289;
DT      01-JUN-1994 (Rel. 29, Created)
DT      01-JUN-1994 (Rel. 29, Last sequence update)
DT      15-DEC-1998 (Rel. 37, Last annotation update)
DE      POSSIBLE 12 KD NUCLEIC ACID-BINDING PROTEIN.
OS      San Miguel sea lion virus (serotype 4) (SMSV 4).
OC      Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
OC      Calicivirus.
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE; 92410750.
RA      Neill J.D.;
RT      "Nucleotide sequence of the capsid protein gene of two serotypes of
RT      San Miguel sea lion viruses: identification of conserved and non-
RT      conserved amino acid sequences among calicivirus capsid proteins.";
RL      Virus Res. 24:211-222(1992).
CC      -1- SIMILARITY: TO FELINE CALICIVIRUS 12 KD PROTEIN.
CC      -----
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CC      -----
DR      EMBL; M87482; AAA16221.1; -.
DR      PIR; D48562; D48562.
SQ      SEQUENCE     110 AA; 12566 MW; 14255D593827A18E CRC64;

Query Match          16.7%; Score 95; DB 1; Length 110;
Best Local Similarity 28.9%; Pred. NO. 8.34e-02;
Matches 13; Conservative 17; Mismatches 13; Indels 2; Gaps 2;

Db      10 FLNSVANAVVEKKDL-ASKGLQLKSRAALDERAFNYDRIAFEK 53
OY      17 FIKRSVNVIITHGRIDIFASKNFHLQNKTIIGRRISL-KLTSCK 60
```

RESULT ID	6	STANDARD:	PRT:	374 AA.
AC	SBP_CRYIA			
DT	P18632;			
DT	01-NOV-1990 (Rel. 16, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	15-DEC-1998 (Rel. 37, Last annotation update)			
DE	SUGI BASIC PROTEIN PRECURSOR (SBP) (MAJOR ALLERGEN CRY J 1) (CRY J 1).			
OS	Cryptomeria japonica (Japanese cedar).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
CC	euphyllophytes; Spermatophyta; Coniferopsida; Coniferales;			
CC	Taxodiaceae; Cryptomeria.			
RN	[1]			
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.			
RC	TISSUE=POLLEN.			
RX	MEDLINE: 94183234.			
RA	Sone T., Komiyama N., Shimizu K., Kusakabe T., Morikubo K.,			
RT	Kino K.;			
RT	"Cloning and sequencing of cDNA coding for Cry j I, a major allergen			
RL	of Japanese cedar pollen.";			
RL	Biochem. Biophys. Res. Commun. 199:619-625(1994).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=POLLEN.			
RA	Namba M., Kurose M., Torioge K., Fukuda S., Kurimoto M.;			
RL	Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.			
RP	SEQUENCE OF 22-41.			
RC	TISSUE=POLLEN.			
RX	MEDLINE: 89031257.			
RA	Tanai M., Ando S., Usui M., Kurimoto M., Sakaguchi M., Inouye S.,			
RT	Mathias T.;			
RT	"N-terminal amino acid sequence of a major allergen of Japanese cedar			
RL	pollen (Cry j I)." ;			
RL	FEBS Lett. 239:329-332(1988).			
RN	[4]			
RP	CARBOHYDRATES.			
RA	MEDLINE: 95003748.			
RA	Hijikata A., Matsumoto I., Kojima K., Ogawa H.;			
RT	"Antigenicity of the oligosaccharide moiety of the Japanese cedar			
RL	(Cryptomeria japonica) pollen allergen, Cry jI." ;			
CC	Int. Arch. Allergy Immunol. 105:198-202(1994).			
CC	-1- PTM: CONTAINS FUCOSE/XyLOSE-CONTAINING N-LINKED OLIGOSACCHARIDS.			
CC	-1- DISEASE: THIS PROTEIN IS THE MAJOR ALLERGEN OF JAPANESE CEDAR			
CC	POLLEN, THE MOST COMMON POLLEN ALLERGEN IN JAPAN.			
CC	-1- MISCELLANEOUS: THE SEQUENCE OF CRY J I FORM A IS SHOWN HERE. FORM			
CC	B DIFFERS IN SIX POSITIONS.			
CC	-1- SIMILARITY: BELONGS TO THE POLYSACCHARIDE LYASE FAMILY 1.			
CC	AMB A I/AMB A II/CRY J I SUBFAMILY.			
CC	-----			
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
CC	-----			
CC	EMBL: D26544; BAA05542.1; -			
DR	EMBL: D26545; BAA05543.1; -			
DR	EMBL: D34639; BAA07020.1; -			
DR	PIR: A44773; A44773.			
DR	PEAM: PF00544; pec_lyase; 1.			
DR	PRINTS: PRO0807; AMBALLERGEN.			
KW	Allergen; Glycoprotein; Multigene family; Signal.			
FT	SIGNAL	1	21	
FT	CHAIN	22	374	
FT	VARIANT	12	12	
FT	VARIANT	143	143	
FT	VARIANT	202	202	
FT	VARIANT	221	221	
FT	VARIANT	358	358	
FT	VARIANT	361	361	
FT	VARIANT	158	158	
FT	CARBOHYD			
FT	POTENTIAL.			

	FT	SO	Query Match	Best Local Similarity	Matches	Score	DB 1:	Length	374:	Pred.	No. 8,34e-02:	Mismatches	0:	Indels	0:	Gaps	0
DB	234	1	16.7%;	100.0%;	13;	95;	DB 1:	374;		0;	8,34e-02;	0;					
QY	1	1	16.7%;	100.0%;	13;	95;	DB 1:	374;		0;	8,34e-02;	0;					
RESULT	7																
ID	KALM_HUMAN	STRAND:	PR:	680	AA.												
AC	P23352;																
DT	01-NOV-1991 (Rel. 20, Created)																
DT	01-DEC-1992 (Rel. 24, Last sequence update)																
DT	01-OCT-1996 (Rel. 34, Last annotation update)																
DE	KALLMANN SYNDROME PROTEIN PRECURSOR (ADHESION MOLECULE-LIKE X-LINKED).																
GN	KALI OR KAL OR ADMXLX OR KALIGI.																
OS	Hum sapiens (Human).																
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;																
OC	Eutheria; Primates; Catarrhini; Homidae; Homo.																
RN	[1]																
RP	SEQUENCE FROM N.A.																
RA	MEDLINE: 92005720.																
RA	Legouis R., Hardelin J.-P., Levilliers J., Claverie J.-M., Compain S.,																
RA	Munderle V., Millaudeau P., le Paslier D., Cohen D., Caterina D.,																
RA	Bougueret L., Delamarre-Van de Waal H., Lutfalla G., Weissenbach J.,																
RA	Petit C.;																
RT	"The candidate gene for the x-linked Kallmann syndrome encodes a																
RT	protein related to adhesion molecules.";																
RL	[Cell 67:423-435(1991).]																
RN	[2]																
RP	REVISIONS:																
RA	MEDLINE: 93265164.																
RA	del Castillo I., Cohen-Salmon M., Blanchard S., Lutfalla G.,																
RA	Petit C.;																
RT	"Structure of the x-linked Kallmann syndrome gene and its homologous																
RT	pseudogene on the Y chromosome.";																
RL	Nat. Genet. 2:305-310(1992).]																
RN	[3]																
RP	SEQUENCE FROM N.A.																
RA	MEDLINE: 92018217.																
RA	Francio B., Gutolfi S., Pragliola A., Inceri B., Bardonì B.,																
RA	Tonlorenzi R., Carrozo R., Maestrini E., Pleretti M.,																
RA	Tailon-Miller P., Brown C.J., Willard H.F., Lawrence C.,																
RA	Pericco N.G., Cernigoi G., Ballabio A.;																
RT	"A gene deleted in Kallmann's syndrome shares homology with neural																
RT	cell adhesion and axonal path-finding molecules.";																
RL	Nature 353:529-536(1991).]																
RN	[4]				</												

HYPOTHALAMIC REGION AS WELL AS THE AXONAL EXTENSION OF OLFACTORY NEURONS TOWARDS THE FOREBRAIN ARE IMPAIRED.

-1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS

-1- SIMILARITY: CONTAINS 1 WAP-TYPE 'FOUR-DISULFIDE CORE' DOMAIN.

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CC

DR EMBL: M97282; AAA59202.1; -

DR EMBL: S60085; AAB20108.1; ALT\_SEQ.

DR EMBL: X60299; CAA42841.1; -

DR EMBL: X82034; CAA57554.1; -

DR PIR: A40351; A40351.

DR PIR: S17982; S17982.

DR MIM: 147950; -

DR MIM: 308700; -

DR PRINTS: PR00003; 4DISULPHCORE.

DR PROSITE: PS00317; 4.DISULFIDE\_CORE; 1.

DR PFAM: PF00041; fn3; 3.

DR PFAM: PF00095; wap; 1.

KW Cell adhesion; Glycoprotein; Serine protease inhibitor; Signal; Polymorphism; Disease mutation.

FT SIGNAL 1 20

FT CHAIN 21 680

FT DOMAIN 21 120

FT DOMAIN 131 176

FT DOMAIN 181 285

FT DOMAIN 286 402

FT DOMAIN 403 540

FT DOMAIN 541 661

FT CARBOHYD 71 71

FT CARBOHYD 209 209

FT CARBOHYD 300 300

FT CARBOHYD 470 470

FT CARBOHYD 553 553

FT CARBOHYD 564 564

FT VARIANT 267 267

FT VARIANT 534 534

FT CONFLICT 70 71

FT CONFLICT 373 373

FT CONFLICT 540 540

SO SEQUENCE 680 AA; 76066 MW; 5D6ACCF14B5F5F8 CRC64;

Query Match

Best Local Similarity 27.1%; Pred. No. 8.34e-02;

Matches 16; Conservative 19; Mismatches 23; Indels 1; Gaps 1;

DB 248 VQLTDIRSR-VQFRVAANVHGRTAPSKFRSSKDPSPAPAPANRLANSTVNS 305

OY 5 VAFNQGPNRVRFTKRVSNVHGRIDIPASKNFHLQNTIGRISLTKLSGRTAS 63

RESULT 8

ID YWJA.BACSU STANDARD; PRT; 575 AA.

AC P45861;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-OCT-1996 (Rel. 34, Last annotation update)

DE HYPOTHEICAL ABC TRANSPORTER ATP-BINDING PROTEIN IN ACDA 5' REGION.

GN YWJA.

OS Bacillus subtilis.

OC Bacteria; Firmicutes; Bacillus/Clostridium group;

OC Bacillus/Staphylococcus group; Bacillus.

RN 11

RP SEQUENCE FROM N.A.

RC STRAIN-168;

RA Glaser P., de la Fuente V., Danchin A.;

RL Submitted (May-1995) to the EMBL/GenBank/DBJ databases.

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).

CC -1- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY (ABC TRANSPORTERS). MSBA SUBFAMILY.

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CC

DR EMBL: 249782; CAA89862.1; -

DR EMBL: 299123; CAB15751.1; -

DR HSSP: P13569; INBD.

DR SUBTILIST: BG11306; YWJA.

DR PROSITE: PS00211; ABC\_TRANSPORTER; 2.

DR PFAM: PF00005; ABC\_tran; 1.

DR PFAM: PF00664; ABC\_membrane; 1.

KW Hypothetical protein; ATP-binding; Transport; Transmembrane.

FT TRANSMEM 16 36

FT TRANSMEM 50 70

FT TRANSMEM 132 152

FT TRANSMEM 154 174

FT TRANSMEM 244 264

FT TRANSMEM 267 287

FT NP\_BIND 366 373

SO SEQUENCE 575 AA; 64562 MW; 0F331439E675C8F4 CRC64;

Query Match

Best Local Similarity 16.5%; Score 94; DB 1; Length 575;

Matches 19; Conservative 17; Mismatches 27; Indels 2; Gaps 2;

DB 176 KMKTKAFTLLNKIDGFSRVENNIGGIRLVOAFGEAEKRFVANNQRFVVT-KLSY 234

OY 1 MKVTAFNQGPNRVRFTKRVSNVHGRIDIPASKNFHLQNTIGRISLTKLSG 59

DB 235 KIMAK 239

OY 60 KIASR 64

RESULT 9

ID G3P2.BACSU STANDARD; PRT; 340 AA.

AC O34425;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE 2 (EC 1.2.1.12) (GAPDH).

GN GAPD.

OS Bacillus subtilis.

OC Bacteria; Firmicutes; Bacillus/Clostridium group;

OC Bacillus/Staphylococcus group; Bacillus.

RN 11

RP SEQUENCE FROM N.A.

RA MEDLINE: 98048467.

RA Lapidus A., Galleron N., Sorokin A., Ehrlich S.D.;

RT "Sequencing and functional annotation of the Bacillus subtilis genes in the 200 kb rtm-dna region."

RL Microbiology 143:3431-3441(1997).

CC -1- CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE + ORTHOPHOSPHATE + NAD(+) = 1,3-DIPHOSPHATEGLYCERATE + NADH.

CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE FAMILY.

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100

100

1

Db 350 YSPGHIFRTIDKGIISNHPFISPSAKY 379  
 QY 10 FGPNRRVFIKRVSNVITIGRIDIFASKNF 39

RESULT 12  
 ID PECK\_AMASU STANDARD: PRT: 532 AA.

DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE PHOSPHOENOLPYRUVATE CARBOXYKINASE [ATP] (EC 4.1.1.49).  
 GN PCKA.  
 OS Anaerobiospirillum succiniciproducens.  
 OC Bacteria; Proteobacteria; gamma subdivision; Succinivibrionaceae;  
 NC Anaerobiospirillum.  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 29305;  
 RX MEDLINE: 97316436.  
 RA Laivenieks M., Vielle C., Zeikus J.G.;  
 RT "Cloning, sequencing, and overexpression of the Anaerobiospirillum  
 succiniciproducens phosphoenolpyruvate carboxykinase (pckA) gene."  
 RL Appl. Environ. Microbiol. 63:2273-2280(1997).  
 CC -1- CATALYTIC ACTIVITY: ATP + OXALOACETATE -> ADP + PHOSPHOENOLPYRUVATE  
 + CO(2).  
 CC -1- PATHWAY: RATE-LIMITING GLUCONEOGENIC ENZYME.  
 CC -1- SIMILARITY: BELONGS TO THE PHOSPHOENOLPYRUVATE CARBOXYKINASE (ATP)  
 FAMILY.

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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL: U95960; AAC45394.1; -  
 DR HSPF: P22259; IOEN.  
 DR PROSITE: PS00532; PEPCK\_ATP; 1.  
 DR PFAM: PF01293; PEPCK\_ATP; 1.  
 KW Glucocoenogenesis; Lyase; Decarboxylase; ATP-binding.  
 FT NP BIND 242  
 FT SEQUENCE 532 AA; 58643 MW; 983ABC71930F9E44 CRC64;

Query Match 15.1%; Score 86; DB 1; Length 532;  
 Best Local Similarity 34.1%; Pred. No. 1,546+00;  
 Matches 15; Conservative 12; Mismatches 16; Indels 1; Gaps 1;

Db 421 KREMSGAKAVYVNTGNGTGKRIKRTGRTIDAI-IDGSIDT 463  
 QY 29 RAIDIFASKNFHLQKNTIGTRISLKLTSGRKISRVDGIITAA 72

RESULT 13  
 ID YH4\_YEAST STANDARD: PRT: 1070 AA.

DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 01-FEB-1995 (Rel. 31, Last annotation update)  
 DE HYPOTHETICAL 123.0 KD PROTEIN IN SP016-REC104 INTERGENIC REGION.  
 GN YHR154W.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;  
 CC Saccharomycetaceae; Saccharomycetes.  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN=S288C / AB972;  
 RX MEDLINE: 94378003.  
 RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,  
 RA Du Z., Favell A., Fulton L., Gattung S., Geisel C., Kirsten J.,

RA Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,  
 RA Latreille P., Louis E.J., Macri C., Maris E., Meneses S., Mouser L.,  
 RA Nham M., Rifkin L., Riles L., St. Peter H., Trevasis E., Vaughan K.,  
 RA Vignati D., Wilcox L., Woldman P., Waterston R., Wilson R.,  
 RA Vaudin M.;  
 RT "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome  
 RT VII."  
 RT Science 265:2077-2082(1994).

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DR EMBL: U10397; AAB6878.1; -  
 DR PIR: S46755; S46755.  
 DR PFAM: PF00533; BRCT; 5.  
 KW Hypothetical protein.  
 SQ SEQUENCE 1070 AA; 123017 MW; 767931285BB52580 CRC64;

Query Match 15.1%; Score 86; DB 1; Length 1070;  
 Best Local Similarity 31.5%; Pred. No. 1,546+00;  
 Matches 17; Conservative 15; Mismatches 20; Indels 2; Gaps 2;

Db 380 LTVAYTFGSGRFYIOLIVE-IIGSLSTPEKRNHLTKSTGKRVYAK 432  
 QY 3 VTAVFNGPFRVRFIKRVSNVITIGRIDIFASKNFHL-QKNTIGTRISL 55

RESULT 14  
 ID YQFA\_BACSU STANDARD: PRT: 331 AA.

AC P54466;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE HYPOTHETICAL 35.6 KD PROTEIN IN RP50-PHOH INTERGENIC REGION.  
 GN YQFA.  
 OS Bacillus subtilis.  
 CC Bacteria; Firmicutes; Bacillus/Clostridium group;  
 OC Bacillus/staphylococcus group; Bacillus.  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN=168 / JH642;  
 RA Kobayashi Y., Mizuno M., Masuda S., Takemaru K., Hosono S.,  
 RA Sato T., Takeuchi M.;  
 RL Submitted (MAY-1996) to the EMBL/Genbank/DDBJ databases.

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DR EMBL: D84432; BA12473.1; -  
 DR EMBL: D99117; CAB14480.1; -  
 DR SUBTILIST; BG11651; YQFA.  
 KW Hypothetical protein; Transmembrane.  
 FT TRANSMEM 6  
 FT TRANSMEM 26  
 FT SEQUENCE 331 AA; 35641 MW; 484AD959F8109A7A CRC64;

Query Match 14.9%; Score 85; DB 1; Length 331;  
 Best Local Similarity 22.8%; Pred. No. 2,106+00;  
 Matches 18; Conservative 29; Mismatches 26; Indels 6; Gaps 6;

Db 39 VKIST-FTLVGRRLRVVNPVPLIAHRAAGLVGTN-QLESHYLAGN-YD-RVVA 94  
 QY 1 KVVTAENFGPN-RRVFIKRVSNVITIGRIDIFASKNFHLQKNTIGTRISL 59



(TM)

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MPsrch\_bp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Jun 19 15:53:07 2000; Maspar time 14.18 Seconds

Tabular output not generated. 391.228 Million cell updates/sec

Title: >US-09-142-524A-1  
Description: (1-80) from US09142524A.pep  
Perfect Score: 569  
Sequence: 1 MKVTVAFNQFGPNRRVFIKR.....IASRRVDGIIMAYONPASWK 80

Scoring table:  
PAM 150  
Gap 11

Searched: 225878 segs, 69334122 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database:

1:sp-archaea 2:sp-bacteria 3:sp-fungi 4:sp-human  
5:sp-invertebrate 6:sp-mammal 7:sp-mmc 8:sp-organelle  
9:sp-phage 10:sp-plant 11:sp-rodent 12:sp-unclassified  
13:sp-vertebrate 14:sp-virus

Statistics: Mean 39.247; Variance 71.415; scale 0.550

Score No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	97	17.0	375	10	Q96385	CHAOI PRECURSOR.	6.15e-02
2	95	16.7	173	5	Q18991	D2085.2 PROTEIN.	1.22e-01
3	95	16.7	367	10	Q92NU7	POLLEN MAJOR ALLERGEN	1.22e-01
4	94	16.5	893	5	O02099	CODED FOR BY C. ELEGAN	1.71e-01
5	91	16.0	1160	5	O27829	PLASMA MEMBRANE CALCIU	4.65e-01
6	89	15.6	190	2	O9X2E7	RIBOTLAVIN SYNTHASE, A	8.96e-01
7	88	15.5	108	14	O09783	CAPSID.	1.24e+00
8	88	15.5	350	2	P73865	SENSOR TRANSDUCTION H	1.71e+00
9	87	15.3	110	14	P89682	CAPSID PROTEIN.	1.71e+00
10	87	15.3	394	10	O65457	PECTATE LYASE LIKE PRO	1.71e+00
11	87	15.3	478	5	O44153	PECTATE LYASE LIKE PRO	1.71e+00
12	86	15.1	440	2	O69661	HYPOTHETICAL 47.7 KD P	2.36e+00
13	86	15.1	586	5	Q17813	ENT-KAURENE SYNTHETASE	2.36e+00
14	86	15.1	802	10	Q38802	ORF 1, ORF 2 AND ORF 3	3.24e+00
15	85	14.9	84	14	O89873	90.8 KD REVERSE TRANSC	4.43e+00
16	85	14.9	790	8	O02718	HYPOTHETICAL 30.0 KD P	4.43e+00
17	84	14.8	270	2	P73013	HYPOTHETICAL 41.5 KD P	4.43e+00
18	84	14.8	360	2	O92GL9	PUTATIVE MITOCHONDRIAL	4.43e+00
19	84	14.8	647	3	O94445		

21	84	14.8	1330	2	O53689	HYPOTHETICAL 145.2 KD	4.43e+00
22	84	14.8	3229	5	Q26912	PROTEIN 1 OF A DISPERS	4.43e+00
23	83	14.6	288	2	O50267	MOAR.	6.05e+00
24	83	14.6	773	10	O80631	FL2L6.10 PROTEIN.	6.05e+00
25	83	14.6	1170	4	O16817	PLASMA MEMBRANE CALCIU	6.05e+00
26	83	14.6	1259	14	O9YKCS	STRUCTURAL POLYPROTEIN	6.05e+00
27	83	14.6	1873	14	O83044	METHYLTRANSFERASE.	6.05e+00
28	83	14.6	2272	5	O17329	GAG, POL AND ENV PROTE	6.05e+00
29	82	14.4	289	5	O01613	COSMID T19H12.	8.25e+00
30	82	14.4	295	6	O28875	BAND 6 POLYPEPTIDE B6P	8.25e+00
31	82	14.4	390	10	O65388	FI2L1.22 PROTEIN.	8.25e+00
32	82	14.4	454	3	P78879	FISTION YEAST (FRAGMEN	8.25e+00
33	82	14.4	497	2	O9ZDUS	HISTIDINE KINASE SENSO	8.25e+00
34	82	14.4	533	5	O01617	HYPOTHETICAL 60.7 KD P	8.25e+00
35	82	14.4	534	5	O18636	ZC44.3.6 PROTEIN.	8.25e+00
36	82	14.4	725	4	O13835	BAND-6-PROTEIN.	8.25e+00
37	82	14.4	726	4	O15152	PLAOPHILIN.	8.25e+00
38	82	14.4	727	6	O28161	ALPHA SUBUNIT OF NITRA	8.25e+00
39	82	14.4	1195	2	O06459	ASPARATE RACEMASE.	8.25e+00
40	81	14.2	232	1	O93779	TRANSPOSASE OF TN10.	1.12e+01
41	81	14.2	402	12	O9WTF5	HYPOTHETICAL 60.9 KD P	1.12e+01
42	81	14.2	534	5	O01614	PLAOPHILIN 1.	1.12e+01
43	81	14.2	728	11	P97350	HYPOTHETICAL 110.9 KD	1.12e+01
44	81	14.2	982	5	O09532	LTR-RETROTRANSPOSON SK	1.12e+01
45	81	14.2	1116	5	O15725		

## ALIGNMENTS

RESULT 1  
ID Q96385; PRELIMINARY; PRT; 375 AA.  
AC Q96385;

DT 01-FEB-1997 (Tremblrel. 02, Created)  
DT 01-FEB-1997 (Tremblrel. 02, Last sequence update)  
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)

DE CHAOI PRECURSOR.  
OS Chamaecyparis obtusa.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
CC Euphyllophytes; Spermatophyta; Coniferopsida; Coniferales;  
CC Taxodiaceae; Chamaecyparis.

RP [1]  
RC SEQUENCE FROM N.A.  
FC TISSUE-POLLEN;  
RX MEDLINE: 96265194.  
RA SUZUKI M., KOMITAMA N., ITOH M., ITOH H., SONE T., KUNO K., TAKAGI I.,  
RA OHTA N.;  
RT "Purification, characterization and molecular cloning of Cha o 1, a  
major allergen of Chamaecyparis obtusa (Japanese cypress) pollen.";  
RL KOL. Immunol. 33:451-460(1996).  
DR EMBL: D45404; BAA08246.1; -;  
DR MENDEL: 7626; Chao; 1088; 7626.  
DR PFAM: PF00544; pec\_lyase; 1.  
DR PRINTS: PRO0807; AMBALDERGEN.  
KW Signal.

FT SIGNAL. 1 21 POTENTIAL.  
FT CHAIN 22 375 CHAO1.  
SQ SEQUENCE 375 AA; 40258 MW; A0981492 CRC32;

Query Match 17.08; Score 97; DB 10; Length 375;  
Best Local Similarity 59.38; Pred. No. 6.15e-02;  
Matches 16; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

DB 234 MKVTVAFNQFGPNRRVFIKRVLH 260  
QY 1 MKVTVAFNQFGPNRRVFIKRVLH 27

RESULT 2  
ID Q18991; PRELIMINARY; PRT; 173 AA.  
AC Q18991;  
DT 01-NOV-1996 (Tremblrel. 01, Created)  
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)  
DT 01-JAN-1999 (Tremblrel. 09, Last annotation update)



DE D2085.2 PROTEIN.  
 CN D2085.2.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;  
 NC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA BAYNES C.;  
 RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 94150718.  
 RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,  
 RA BONFIELD J., BURTON J., CONNELL M., COPEY T., COOPER J., COULSON A.,  
 RA CRAYTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,  
 RA GARDNER A., GREEN P., KIRSTEN J., LAISTER N., LATREILLE P.,  
 RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LAURELLE P.,  
 RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,  
 RA PARSONS J., PERCY C., RIEKEN L., ROOPRA A., SAUNDERS D., SHONKKEEN R.,  
 RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULLSTON J.,  
 RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,  
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHDMAN P.;  
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
 elegans.";  
 RL Nature 368:32-38(1994).  
 DR EMBL: 254284; CA91060.1; -  
 SQ SEQUENCE 173 AA; 20523 MW; 6884DF8F CRC32;  
 Query Match 16.7%; Score 95; DB 5; Length 173;  
 Best Local Similarity 24.7%; Pred. No. 1,22e-01;  
 Matches 19; Conservative 23; Mismatches 29; Indels 6; Gaps 5;  
 Db 6 QFDEIRGFVQKNNENFHWOLKEVFSNNOMLFRLNSIQIKYARETLKLSGRTV 65  
 QY 9 QFGFNRRVFVKRSVNIHGRIDIFASKN--FHLQKN-TIGT-GRRISLK-LTSGKIAS 63  
 Db 66 SETHILYNTQYPTTM 82  
 QY 64 RRVGGII-AAVQNPASW 79  
 RESULT 3 PRELIMINARY; PRT; 367 AA.  
 ID Q92NUT;  
 AC Q92NUT;  
 DT 01-MAY-1999 (TREMBlrel. 10, Created)  
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)  
 DE POLLEN MAJOR ALLERGEN 1-2.  
 OS Juniperus ashei (Ozark white cedar).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC euphyllophytes; Spermatophyta; Coniferopsida; Coniferales;  
 OC Taxodiaceae; Juniperus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MIDORO-HORIIUTI T.M., GOLDBLUM R.M., KUROSKI A., WOOD T.G.,  
 RA BROOKS E.G.;  
 RT "Molecular cloning of mountain cedar (Juniperus ashei) pollen major  
 RT allergen, Jun a 1.";  
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF106663; AAD03609.1; -  
 DR EMBL: AF106662; AAD03608.1; -  
 DR MENDEL: 36544; Junas:1088; 36544.  
 DR MENDEL: 36545; Junas:1088; 36545.  
 SQ SEQUENCE 367 AA; 39824 MW; 4C2DB630 CRC32;  
 Query Match 16.7%; Score 95; DB 10; Length 367;  
 Best Local Similarity 100.0%; Pred. No. 1,22e-01;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 234 MKVTAFNPGFN 246  
 QY 1 MKVTAFNPGFN 13

RESULT 4  
 ID 002099 PRELIMINARY; PRT; 893 AA.  
 AC 002099;  
 DT 01-JUL-1997 (TREMBlrel. 04, Created)  
 DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)  
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)  
 DE CODED FOR BY C. ELEGANS CDNA YK23C8.3.  
 GN C18B3.3.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;  
 OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RX MEDLINE: 94150718.  
 RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,  
 RA BONFIELD J., BURTON J., CONNELL M., COPEY T., COOPER J., COULSON A.,  
 RA CRAYTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,  
 RA GARDNER A., GREEN P., KIRSTEN J., LAISTER N., LAURELLE P.,  
 RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LAURELLE P.,  
 RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,  
 RA PARSONS J., PERCY C., RIEKEN L., ROOPRA A., SAUNDERS D., SHONKKEEN R.,  
 RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULLSTON J.,  
 RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,  
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHDMAN P.;  
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
 elegans.";  
 RL Nature 368:32-38(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RA CONNELL M., MAGGI L.;  
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RA WATERSTON R.;  
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF000265; AAB52941.1; -  
 SQ SEQUENCE 893 AA; 102424 MW; 696AF324 CRC32;  
 Query Match 16.5%; Score 94; DB 5; Length 893;  
 Best Local Similarity 31.3%; Pred. No. 1,71e-01;  
 Matches 20; Conservative 20; Mismatches 20; Indels 4; Gaps 4;  
 Db 602 VSLKATNVPRAP-FWYSTRKNLEHLSTPEYTPARRISLOFPLKISNQPD-IFKQY 659  
 QY 16 VFIRKSVNIHGRIDIFASKN-F-HLQKNITGTGRISLKLTSGKIASRVGGIIAAV 73  
 Db 660 HLPT 663  
 QY 74 QNPA 77  
 RESULT 5 PRELIMINARY; PRT; 1160 AA.  
 ID Q27829;  
 AC Q27829;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)  
 DE PLASMA MEMBRANE CALCIUM ATPASE.  
 OS Parametium tetraurelia  
 OC Eukaryota; Alveolata; Ciliophora; Nassophorea; Penicillula; Parametium.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-51S;  
 RA ELWESS N.L., VAN HOUTEN J.L.;  
 RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U05880; AAB81284.1; -  
 DR PROSITE: P800154; ATPASE\_EL\_E2; 1.  
 DR PFAM: PF00122; E1-E2-ATPase; 2.  
 DR PRINTS: PR00119; CATALYPASE.



KM Hydrolase; Transmembrane; Phosphorylation; ATP-binding.  
 FT MOD.RES 442 442 PHOSPHORYLATION (PROBABLE).  
 SQ SEQUENCE 1160 AA; 130984 MW; 68C09A2D CRC32;

Query Match 16.0%; Score 91; DB 5; Length 1160;  
 Best Local Similarity 26.8%; Pred. No. 4,65e-01;  
 Matches 15; Conservative 16; Mismatches 22; Indels 3; Gaps 3;

Db 543 MSVVDTHNGHGLPVKRLVKGASLIVSLTHMTYDDOKLKGVDIQLERIS 598  
 1 MKVTAFFNOFG-PNRVRFKRVSNVTHG-RRIDFASKNFHLQ-KNITIGRRIS 53

RESULT 6  
 ID Q9X2E7 PRELIMINARY; PRT; 190 AA.

DT 01-NOV-1999 (Tremblrel. 12, Created)  
 DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)  
 DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)  
 DE RIBOFLAVIN SYNTHASE, ALPHA SUBUNIT.  
 GN TM1827.  
 OS Thermotoga maritima.  
 OC Bacteria; Thermotogales; Thermotoga.

RP SEQUENCE FROM N.A.  
 RX MEDLINE: 99287316.  
 RA NELSON K.E., CLAYTON R.A., GILL S.R., GWINN M.L., DODSON R.J.,  
 RA HAFT D.H., HICKY E.K., PETERSON J.D., NELSON W.C., KETCHUM K.A.,  
 RA MCDONALD L., UTTERBACK T.R., MALEK J.A., LINER K.D., GARRETT M.M.,  
 RA STEWART A.M., COTTON M.D., PRATT M.S., PHILLIPS C.A., RICHARDSON D.,  
 RA HEIDELBERG J., SUTTON G.G., FLEISCHMANN R.D., WHITE O., SALZBERG S.L.,  
 RA SMITH H.O., VENTER J.C., FRASER C.M.,  
 RT "Evidence for lateral gene transfer between Archaea and bacteria from  
 RT genome sequence of *Thermotoga maritima*.";  
 RL Nature 399:323-329(1999).  
 RN [2]

RP SEQUENCE FROM N.A.  
 RA NELSON K.E., CLAYTON R.A., GILL S.R., GWINN M.L., DODSON R.J.,  
 RA HAFT D.H., HICKY E.K., PETERSON J.D., NELSON W.C., KETCHUM K.A.,  
 RA MCDONALD L., UTTERBACK T.R., MALEK J.A., LINER K.D., GARRETT M.M.,  
 RA STEWART A.M., COTTON M.D., PRATT M.S., PHILLIPS C.A., RICHARDSON D.,  
 RA HEIDELBERG J., SUTTON G.G., FLEISCHMANN R.D., WHITE O., SALZBERG S.L.,  
 RA SMITH H.O., VENTER J.C., FRASER C.M.,  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AEO01819; AAD36890.1; -  
 SQ SEQUENCE 190 AA; 21678 MW; F999479B CRC32;

Query Match 15.6%; Score 89; DB 2; Length 190;  
 Best Local Similarity 28.6%; Pred. No. 8,96e-01;  
 Matches 10; Conservative 13; Mismatches 11; Indels 1; Gaps 1;

Db 60 RTNLFVSRFYNLEK-SIALGSRVHGHWGHD 93  
 29 RRIDFASKNFHLQKNITIGRRISLKTSGKIAS 63

RESULT 7  
 ID Q09783 PRELIMINARY; PRT; 108 AA.

AC Q09783; 009783;  
 DT 01-JUL-1997 (Tremblrel. 04, Created)  
 DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)  
 DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)  
 DE CAPSID.  
 OS San Miguel sea lion virus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;  
 OC Calicivirus.  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN-SMRY-17;  
 RA MEDLINE: 98187296.  
 RA MATSON D.O., BERKE T., DINTLOS M.B., POET S.E., ZHONG W.M., DAI X.M.,  
 RA JIANG X., GOLDING B., SMITH A.W.,  
 RT "Partial characterization of the genome of nine animal

RT caliciviruses.";  
 RL Arch. Virol. 141:2443-2456(1996).  
 DR EMBL: U52005; AAC57041.1; -  
 SQ SEQUENCE 108 AA; 12354 MW; 476A3E95 CRC32;

Query Match 15.5%; Score 88; DB 14; Length 108;  
 Best Local Similarity 35.3%; Pred. No. 1,24e+00;  
 Matches 12; Conservative 12; Mismatches 9; Indels 1; Gaps 1;

Db 10 FLNGVANAIEGKIDL-ASKGLOLRALDTER 42  
 17 FIKRVSNVHIGRRIDFASKNFHLQKNITIGRR 50

RESULT 8  
 ID P73865 PRELIMINARY; PRT; 350 AA.

AC P73865;  
 DT 01-FEB-1997 (Tremblrel. 02, Created)  
 DT 01-FEB-1997 (Tremblrel. 02, Last sequence update)  
 DT 01-JAN-1999 (Tremblrel. 09, Last annotation update)  
 DE SENSOR TRANSDUCTION HISTIDINE KINASE.  
 OS Synechocystis sp. (strain PCC 6803).  
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN-PCC6803;  
 RA TABATA S.,  
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]

RP SEQUENCE FROM N.A.  
 RC STRAIN-PCC6803;  
 RX MEDLINE: 97061201.  
 RA KANEKO T., SAITO S.,  
 RA MIYAJIMA N., HIROKAWA M., SUGIURA M., SASAKI T., KIMURA T.,  
 RA HOSOUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NARUO K., OKUMURA S.,  
 RA SHIMPO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASUDA M.,  
 RA TABATA S.,  
 RT "Sequence analysis of the genome of the unicellular cyanobacterium  
 RT Synechocystis sp. strain PCC6803. II. Sequence determination of the  
 RL entire genome and assignment of potential protein-coding regions.";  
 RL DNA Res. 3:109-136(1996).  
 DR EMBL: D90910; BAA1927.1; -  
 DR FRAM: PF00512; signal; 1.  
 SQ SEQUENCE 350 AA; 39445 MW; EEF2A0B CRC32;

Query Match 15.5%; Score 88; DB 2; Length 350;  
 Best Local Similarity 38.6%; Pred. No. 1,24e+00;  
 Matches 17; Conservative 12; Mismatches 11; Indels 4; Gaps 2;

Db 246 QRVFNMLTNAIINSPGRKVEISLTSKNNHFOYQVDEGRGIP 289  
 14 RRVFIKRVSNVHIGRRIDFASKNFHLQKNITIGRRIS 53

RESULT 9  
 ID P89682 PRELIMINARY; PRT; 110 AA.

AC P89682;  
 DT 01-MAY-1997 (Tremblrel. 03, Created)  
 DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)  
 DT 01-AUG-1998 (Tremblrel. 07, Last annotation update)  
 DE CAPSID PROTEIN.  
 OS Vesicular exanthema of swine virus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;  
 OC Calicivirus.  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN-A48;  
 RA NEILL J.D., MEYER R.F., SEAL B.S.,  
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U76874; AAC13890.1; -  
 SQ SEQUENCE 110 AA; 12649 MW; 2998BA4B CRC32;

Query Match 15.3%; Score 87; DB 14; Length 110;

Best Local Similarity 28.6%; Pred. No. 1.71e+00;  
Matches 12; Conservative 17; Mismatches 11; Indels 2; Gaps 2;

Db 10 FLNRYANAAGKRLD-ASRGLRSLALDTERDFNAXIA 50  
Matches 11; Conservative 11; Mismatches 0; Indels 0; Gaps 0;  
QY 17 FIKRVSNIHGRIDIFASKNHLKNTIGTGRISL-KLT 57

RESULT 10 PRELIMINARY; PRT; 394 AA.

AC 065457; (TREMBLREL. 07, Created)  
DT 01-AUG-1998 (TREMBLREL. 07, Last sequence update)  
DT 01-NOV-1998 (TREMBLREL. 12, Last annotation update)  
DE PECCATE LYASE LIKE PROTEIN.  
GN FIN20.190.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC eumphylophytes; Spermatophyta; Magnoliophyta; eudicotyledons;  
OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;  
OC Arabidopsis.  
RN [1]  
RA BEVAN M., WEDLER H., WAMBUTT R., BANCROFT I., MEMES H.W., MAYER K.,  
RA SCHUELLER C.;  
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RA EU ARABIDOPSIS SEQUENCING PROJECT;  
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AL022140; CAA18112.1; -  
DR MENDEL; 29068; Arab:1088;29068.  
DR PFAM: PF00544; pec\_lyase.1  
DR PRINTS: PR00807; AMBALBERGEN.  
KW Lyase.  
SQ SEQUENCE 394 AA; 43299 MW; 8B9A93C9 CRC32;

Query Match 15.3%; Score 87; DB 10; Length 394;  
Best Local Similarity 91.7%; Pred. No. 1.71e+00;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 256 MKYVAFNHFPG 267  
QY 1 MKYVAFNHFPG 12

RESULT 11 PRELIMINARY; PRT; 394 AA.

AC 065456; (TREMBLREL. 07, Created)  
DT 01-AUG-1998 (TREMBLREL. 07, Last sequence update)  
DT 01-NOV-1998 (TREMBLREL. 12, Last annotation update)  
DE PECCATE LYASE LIKE PROTEIN.  
GN FIN20.180.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC eumphylophytes; Spermatophyta; Magnoliophyta; eudicotyledons;  
OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;  
OC Arabidopsis.  
RN [1]  
RA BEVAN M., WEDLER H., WAMBUTT R., BANCROFT I., MEMES H.W., MAYER K.,  
RA SCHUELLER C.;  
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RA EU ARABIDOPSIS SEQUENCING PROJECT;  
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AL022140; CAA18111.1; -  
DR MENDEL; 29747; Arab:1088;29747.  
DR PFAM: PF00544; pec\_lyase.1.  
DR PRINTS: PR00807; AMBALBERGEN.  
KW Lyase.

SQ SEQUENCE 394 AA; 43476 MW; 95399178 CRC32;

Query Match 15.3%; Score 87; DB 10; Length 394;  
Best Local Similarity 91.7%; Pred. No. 1.71e+00;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 256 MKYVAFNHFPG 267  
QY 1 MKYVAFNHFPG 12

RESULT 12 PRELIMINARY; PRT; 478 AA.

AC 044153; (TREMBLREL. 06, Created)  
DT 01-JUN-1998 (TREMBLREL. 06, Last sequence update)  
DT 01-NOV-1998 (TREMBLREL. 08, Last annotation update)  
DE C49A9.3 PROTEIN.  
GN C49A9.3.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;  
OC Rhabditina; Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.  
RN [1]  
RA SEQUENCE FROM N.A.  
RC MEDLINE: 94150718.  
RX WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BEERS M.,  
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,  
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,  
RA GARDNER A., GREEN P., HARKINS T., LAYSTER N., LATELLE P.,  
RA JONES M., KERSHAW J., KIRSTEN J., MORTIMORE B., O'CALLAGHAN M.,  
RA LIGHNING J., LLOYD C., MCGRATH A., MORRIS D., O'CALLAGHAN M.,  
RA PARSONS J., PERCY C., RIFKEN L., KOOPRA A., SANDERS D., SHOWNKEEN R.,  
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULLIVAN J.,  
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,  
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,  
RA "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
RT elegans."  
RT Nature 368:32-38(1994).  
RN [2]  
RA SEQUENCE FROM N.A.  
RC STRAIN-BRISTOL N2;  
RX FULTON B., WOHLDMANN P.;  
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RA SEQUENCE FROM N.A.  
RC STRAIN-BRISTOL N2;  
RX WATERSTON R.;  
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF036693; AAB88336.1; -  
SQ SEQUENCE 478 AA; 55107 MW; AC660609 CRC32;

Query Match 15.3%; Score 87; DB 5; Length 478;  
Best Local Similarity 22.9%; Pred. No. 1.71e+00;  
Matches 11; Conservative 20; Mismatches 15; Indels 2; Gaps 2;

Db 207 IQYFALSKPPTPRNVEHIGFIVTVAKLN-VEKDLIFQNNLFG 253  
QY 1 MKYVAFNHFPGNRKVFIRKVSNIHGR-RIDIFASKNHLKNTIG 47

RESULT 13 PRELIMINARY; PRT; 440 AA.

AC 069661; (TREMBLREL. 07, Created)  
DT 01-AUG-1998 (TREMBLREL. 07, Last sequence update)  
DT 01-NOV-1998 (TREMBLREL. 08, Last annotation update)  
DE HYPOTHETICAL 47.7 KD PROTEIN.  
GN MT025.041.  
OS Mycobacterium tuberculosis.  
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN-H37RV;  
 RA BADCOCK K., CHURCHER C.M.;  
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-H37RV;  
 RA BROSCHE R., PARKHILL J., BARRELL B.G., RAJANDREAN M.A.;  
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-H37RV;  
 RA MEDLINE: 96181548.  
 RA PHILIPP W.J., POULET S., EIGMEIER K., PASCOPELLA L.,  
 RA BALASUBRAMANIAN V., HEYM B., BERGH S., BLOOM B.R., JACOBS W.R. JR.,  
 RA COLE S.T.;  
 RT "An integrated map of the genome of the tubercle bacillus,  
 RT Mycobacterium tuberculosis H37RV, and comparison with Mycobacterium  
 RT leprae.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 93:3132-3137(1996).  
 DR EMBL: AL022121; CAI8015.1; -.  
 KM Hypothetical protein.  
 SQ SEQUENCE 440 AA; 47687 MW; 608523P4 CRC32;

Query Match 15.1%; Score 86; DB 2; Length 440;  
 Best Local Similarity 36.7%; Pred. No. 2.36e+00;  
 Matches 11; Conservative 11; Mismatches 7; Indels 1; Gaps 1;  
 DB 227 RRVYLDIGRMAAGRV-GVDTADDPAGW 255  
 OY 50 RRLSLKTSKISRRVDCIIMAYQNPASW 79

RESULT 14  
 ID 017813; PRELIMINARY; PRT; 586 AA.  
 AC 017813;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)  
 DE C08B6.1 PROTEIN.  
 GN C08B6.1.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;  
 OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA WILKINSON J.;  
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE: 94150718.  
 RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,  
 RA BOUNFIELD J., BURTON J., CONNELL M., CORSEY T., COOPER J., COULSON A.,  
 RA CRAXTON M., DEAR S., DU Z., DUBREIN R., FAVELLO A., FULTON L.,  
 RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,  
 RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,  
 RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,  
 RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHANKS R.,  
 RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,  
 RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,  
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;  
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
 RT elegans.";  
 RL Nature 368:32-38(1994).  
 DR EMBL: Z72502; CA96584.1; -.  
 DR PFM: PFO0201; UDPGT; 1.  
 SQ SEQUENCE 586 AA; 67197 MW; DE2A3A87 CRC32;

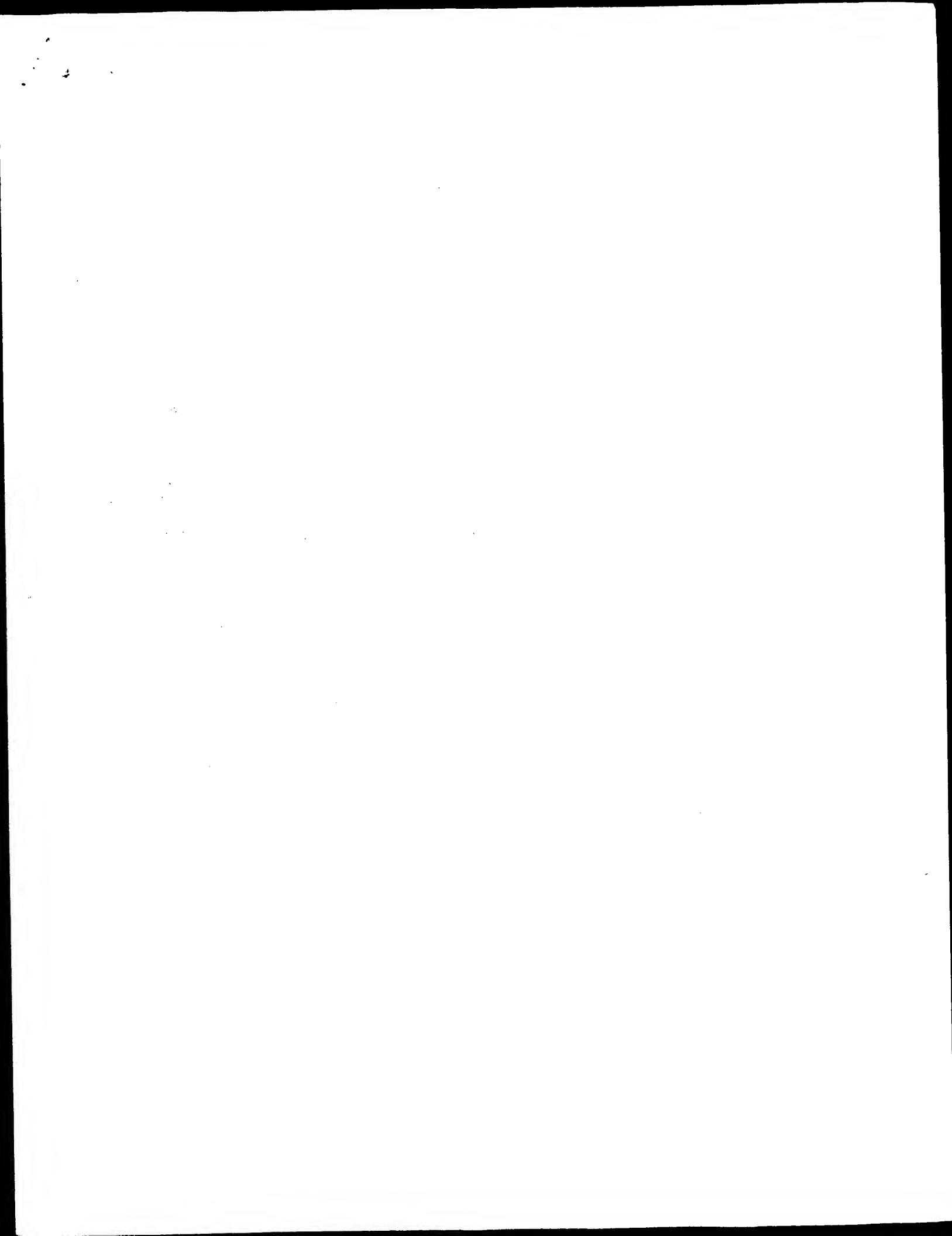
Query Match 15.1%; Score 86; DB 5; Length 586;  
 Best Local Similarity 24.5%; Pred. No. 2.36e+00;  
 Matches 13; Conservative 21; Mismatches 15; Indels 4; Gaps 4;  
 DB 22 KLVF-FNPARGASHNFIKISIDILIDAGHDVIMLPIIAMQKHLVGS-KKV 72

OY 2 KTVAFENO-FGPNRRVFTIKRVSNVITH-GRRIDIFASKNFHLKNTIGTGRRI 52

RESULT 15  
 ID 038802; PRELIMINARY; PRT; 802 AA.  
 AC 038802;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)  
 DE ENT-KAURENE SYNTHETASE A.  
 GN GAL OR T538.9.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;  
 OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;  
 OC Arabidopsis.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-COLUMBIA;  
 RX MEDLINE: 95086384.  
 RA SUN T.P., KAMITA Y.;  
 RT "The Arabidopsis GAL locus encodes the cyclase ent-kaurene synthetase  
 RT A of gibberellin biosynthesis.";  
 RL Plant Cell 6:1509-1518(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC DE LA BASTIDE M., GNOU L., HABERMANN K., HUANG E.N., GOTTESMAN T.,  
 RA KAPLAN N., LODHI M., JENSEN K., HAMEED A., SCHUTZ K., MARIENSSSEN R.,  
 RA DEBHA N., PARNELL L.D., MCCOMBIE W.R.;  
 RT "Arabidopsis thaliana BAC T538 from chromosome IV, short arm.";  
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U11034; AAA53632.1; -.  
 DR EMBL: AC004044; AAD13534.1; -.  
 DR MENDEL, 7142; Arabid; 1532; 7142.  
 DR PFM: PFO1397; Terpene-synth; 1.  
 SQ SEQUENCE 802 AA; 93013 MW; 9AA5783B CRC32;

Query Match 15.1%; Score 86; DB 10; Length 802;  
 Best Local Similarity 24.0%; Pred. No. 2.36e+00;  
 Matches 12; Conservative 18; Mismatches 18; Indels 2; Gaps 2;  
 DB 595 ISSSFGSSDPSRRSFSDQFHEYIANARSDHFNDRNMRLDPGSGVQAR 644  
 OY 3 VTVAFNFGPNRRVFTIKRVSNVITHGRRIDT-FASKNFHLK-NTIGTGR 50

Search completed: Mon Jun 19 15:53:26 2000  
 Job time: 19 secs.



# MUSE

(TM)

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Msrch\_p protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Jun 19 15:57:27 2000; MasPar time 4.99 Seconds

Tabular output not generated. 379.415 Million cell updates/sec

Title: >US-09-142-524A-1  
Description: (1-80) from US09142524A.pep  
Perfect Score: 569

Sequence: 1 MKVTVAFNQFGPNRRVFIRK.....IASRRVDGIIAAYONPASWK 80

Scoring table: PAM 150  
Gap 11

Searched: 188963 segs, 23686106 residues

Post-processing: Minimum Match 0%  
List first 45 summaries  
Maximum DB seq length 80

Database: a-censseq35  
Kgeneseqp

Statistics: Mean 27.708; Variance 116.071; scale 0.239

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	569	100.0	80	1	W27369	Multi-epitope peptide
2	128	22.5	47	1	W80357	Sugi allergen protein
3	117	20.6	17	1	W80347	Sugi allergen protein
4	117	20.6	33	1	W80339	Sugi allergen protein
5	115	20.2	17	1	R81582	Cedar pollen allergen
6	111	19.5	17	1	W80345	Sugi allergen protein
7	111	19.5	17	1	R81580	Cedar pollen allergen
8	107	18.8	15	1	R97884	Japan cedar pollen mat
9	107	18.8	15	1	W57760	Residues 66-80 of Cry
10	106	18.6	47	1	W80350	Sugi allergen protein
11	103	18.1	35	1	W80342	Sugi allergen protein
12	103	18.1	35	1	W57764	Residues 186-200 of Cr
13	98	17.2	15	1	R97908	Japan cedar pollen mat
14	98	17.2	15	1	R97907	Residues 181-195 of Cr
15	98	17.2	15	1	W57763	Cry j I pollen allergen
16	97	17.0	30	1	R45588	Residues 211-225 of Cr
17	95	16.7	15	1	W57755	Japanese cedar pollen
18	95	16.7	15	1	R89293	Sugi allergen protein
19	95	16.7	17	1	W80349	Cry j I pollen allergen
20	95	16.7	20	1	R45563	Cry j I Japanese Cedar
21	95	16.7	20	1	R82512	
22	95	16.7	20	1	R82512	

23	95	16.7	26	1	R45594	Cry j I pollen allergen	4.03e+00
24	95	16.7	28	1	R45590	Cry j I pollen allergen	4.03e+00
25	95	16.7	30	1	W44687	T-cell epitope peptide	4.03e+00

Note: Post-processor removed 20 summaries from list due to search parameters chosen.

## ALIGNMENTS

RESULT 1  
ID W27369 standard; peptide: 80 AA.  
AC W27369:  
DE 24-MAR-1998 (first entry)  
DE Multi-epitope peptide used as immunotherapeutic agent #1.  
KW Multi-epitope peptide; immunotherapeutic agent; allergic disease;  
KW T-cell epitope region; allergen; lymphocyte; immunoglobulin E.  
OS Synthetic.  
PN W09732600-A1.  
PD 12-SEP-1997.  
PR 10-MAR-1997; J00740.  
PR 10-MAR-1996; JP-080702.  
PI (MEIP) MEIJI MILK PROD CO LTD.  
PI Dairiki K, Iwama A, Kuno K, Kume A, Sone T;  
DR WPI: 97-470495/43.  
PT Peptide immuno:therapeutic agent to treat allergic diseases -  
PT contains multi-epitope peptide containing T cell epitope regions  
PT from different allergens  
PS Claim 6; Page 31; 58pp; Japanese.  
CC The present sequence represents a multi-epitope peptide which is used as  
CC or more different allergens (preferably linked via arginine or lysine  
CC dimers), where the T cell epitope regions have a positivity index  
CC greater than 100 as measured in a patient group responding to the  
CC allergen; have at least 70% reactivity with lymphocytes from patients  
CC responding to the allergen; and are not reactive with immunoglobulin E  
CC (IGE) antibodies from patients responsive to the allergen. The agent can  
CC be used to prevent and treat a wide variety of allergic diseases, e.g. by  
CC desensitisation. Side effects, e.g. those mediated by IGE, are reduced.  
SO Sequence 80 AA:

Query Match 100.0%; Score 569; DB 1; Length 80;  
Best Local Similarity 100.0%; Pred. No. 5.38e+45;  
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MKVTVAFNQFGPNRRVFIRKVSNIHGRRIDIFASKNFHLQNTIGTRISLKTSGK 60  
QY 1 MKVTVAFNQFGPNRRVFIRKVSNIHGRRIDIFASKNFHLQNTIGTRISLKTSGK 60  
Db 61 IASRRVDGIIAAYONPASWK 80  
QY 61 IASRRVDGIIAAYONPASWK 80

RESULT 2  
ID W80357 standard; peptide: 47 AA.  
AC W80357:  
DE 11-JAN-1999 (first entry)  
DE Sugi allergen protein Cryj1 derived epitope for T cells.  
KW T cell epitope; sugi allergen proteins Cryj1; Cryj2; treatment;  
KW sugi-pollinosis; allergic reaction; pollen.  
OS Synthetic.  
PN J10259198-A.  
PD 29-SEP-1998.  
PR 22-DEC-1997; 353448.  
PR 24-DEC-1996; JP-343441.  
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.  
PA (SANT) SANKYO CO LTD.  
DR WPI: 98-577037/49.  
PT A linked T cell epitope peptide - used for the treatment of  
PT sugi-pollinosis  
PS Claim 10; Page 5; 21pp; Japanese.  
CC W80339-58 represent epitopes for T cells, derived from the sugi allergen  
CC proteins Cryj1 (W80339-44), W80350-53 and W80356-58) and Cryj2 (W80345-49

CC and W80354-55). The peptides are useful for the treatment of  
CC sugi-pollinosis, an allergic reaction of the body to pollen.  
SQ Sequence 47 AA;

Query Match 22.5%; Score 128; DB 1; Length 47;  
Best Local Similarity 84.0%; Pred. No. 7.58e-03;  
Matches 21; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

DB 12 KLTSGKIASC-LNGIIAAYONPASM 35  
||||||| : : : : :  
QY 55 KLTSGKIASRNVDCIITAYONPASM 79

RESULT 3  
ID W80347 standard; peptide; 17 AA.

AC W80347;  
DT 11-JAN-1999 (first entry)  
DE Sugi allergen protein Cryj2 derived epitope for T cells.  
KW T cell epitope; sugi allergen proteins Cryj1; Cryj2; treatment;  
KM sugi-pollinosis; allergic reaction; pollen.  
OS Synthetic.  
PN J10259198-A.  
PD 29-SEP-1998.  
PF 22-DEC-1997; 353448.  
PR 24-DEC-1996; JP-343441.  
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.  
PA (SANY) SANKYO CO LTD.  
DR WPI: 98-577037/49.  
PT A linked T cell epitope peptide - used for the treatment of  
PT sugi-pollinosis  
PS Claim 7; Page 18; 21pp; Japanese.  
CC W80339-58 represent epitopes for T cells, derived from the sugi allergen  
CC proteins Cryj1 (W80339-44, W80350-53 and W80356-58) and Cryj2 (W80345-49  
CC and W80354-55). The peptides are useful for the treatment of  
CC sugi-pollinosis, an allergic reaction of the body to pollen.  
SQ Sequence 17 AA;

Query Match 20.6%; Score 117; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.45e-02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 IDIFASKNFHLOKNTIG 17  
||||||| : : : : :  
QY 31 IDIFASKNFHLOKNTIG 47

RESULT 4  
ID W80339 standard; peptide; 33 AA.

AC W80339;  
DT 11-JAN-1999 (first entry)  
DE Sugi allergen protein Cryj1 derived epitope for T cells.  
KW T cell epitope; sugi allergen proteins Cryj1; Cryj2; treatment;  
KM sugi-pollinosis; allergic reaction; pollen.  
OS Synthetic.  
PN J10259198-A.  
PD 29-SEP-1998.  
PF 22-DEC-1997; 353448.  
PR 24-DEC-1996; JP-343441.  
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.  
PA (SANY) SANKYO CO LTD.  
DR WPI: 98-577037/49.  
PT A linked T cell epitope peptide - used for the treatment of  
PT sugi-pollinosis  
PS Claim 10; Page 5; 21pp; Japanese.  
CC W80339-58 represent epitopes for T cells, derived from the sugi allergen  
CC proteins Cryj1 (W80339-44, W80350-53 and W80356-58) and Cryj2 (W80345-49  
CC and W80354-55). The peptides are useful for the treatment of  
CC sugi-pollinosis, an allergic reaction of the body to pollen.  
SQ Sequence 33 AA;

Query Match 20.6%; Score 117; DB 1; Length 33;  
Best Local Similarity 67.7%; Pred. No. 6.45e-02;  
Matches 21; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

DB 1 FASKNFHLOKNTIGTAAYONPASKITSGKIAS 31  
||||||| : : : : :  
QY 34 FASKNFHLOKNTIGTG-RRISLKTSGKIAS 63

RESULT 5  
ID R81582 standard; Peptide; 17 AA.

AC R81582;  
DT 24-MAY-1996 (first entry)  
DE Cedar pollen allergen peptide 10 (T-cell epitope).  
KW Cedar; Cryptomeria japonica; pollen; allergen; immunoglobulin E;  
KM Ige: T-cell epitope; antibody; pollinosis; therapy; immunotherapy.  
OS Synthetic.  
PN EP-700929-A2.  
PD 13-MAR-1996.  
PF 08-SEP-1995; 306295.  
PR 10-SEP-1994; JP-242137.  
PR 14-JUL-1995; JP-200221.  
PR 14-JUL-1995; JP-200204.  
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.  
PI Hino K, Saito S, Taniguchi Y;  
DR WPI: 96-140976/15.  
PT New peptide(s) derived from cedar pollen allergens - activate  
PT allergen-specific T-cells, but not allergen-specific IgE antibodies,  
PS used for treating cedar pollinosis  
PS Claim 4; Page 28; 36pp; English.  
CC Synthetic peptides based on portions of cedar pollen allergens A  
CC (R81586) and B (R81587) were tested for their ability to activate  
CC cedar allergen-specific T-cells, but not allergen-specific IgE  
CC antibodies. 6 Peptides (R81580-R81585) were identified as T-cell  
CC epitopes. These peptides, plus subsequences (R81573-79) essential  
CC for T-cell recognition, and homologous peptides (R81588-96) can  
CC be used as immunotherapeutic agents to treat or prevent cedar  
CC pollinosis, avoiding side-effects such as anaphylaxis.  
SQ Sequence 17 AA;

Query Match 20.2%; Score 115; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.47e-02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 DIPASKNFHLOKNTIGT 17  
||||||| : : : : :  
QY 32 DIPASKNFHLOKNTIGT 48

RESULT 6  
ID W80345 standard; peptide; 17 AA.

AC W80345;  
DT 11-JAN-1999 (first entry)  
DE Sugi allergen protein Cryj2 derived epitope for T cells.  
KW T cell epitope; sugi allergen proteins Cryj1; Cryj2; treatment;  
KM sugi-pollinosis; allergic reaction; pollen.  
OS Synthetic.  
PN J10259198-A.  
PD 29-SEP-1998.  
PF 22-DEC-1997; 353448.  
PR 24-DEC-1996; JP-343441.  
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.  
PA (SANY) SANKYO CO LTD.  
DR WPI: 98-577037/49.  
PT A linked T cell epitope peptide - used for the treatment of  
PT sugi-pollinosis  
PS Claim 7; Page 18; 21pp; Japanese.  
CC W80339-58 represent epitopes for T cells, derived from the sugi allergen  
CC proteins Cryj1 (W80339-44, W80350-53 and W80356-58) and Cryj2 (W80345-49  
CC and W80354-55). The peptides are useful for the treatment of  
CC sugi-pollinosis, an allergic reaction of the body to pollen.  
SQ Sequence 17 AA;

Query Match 19.5%; Score 111; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 2.03e-01;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 KVDGIITAYONPASMWK 16  
 :|||||  
 QY 65 RVDGIITAYONPASMWK 80

RESULT 7  
 ID R81580 standard; peptide; 17 AA.  
 AC R81580;  
 DT 24-MAY-1996 (first entry)  
 DE Cedar pollen allergen peptide 8 (T-cell epitope).  
 KW Cedar; Cryptomeria japonica; pollen; allergen; immunoglobulin E;  
 KM IGE: T-cell epitope; antibody; pollinosis; therapy; immunotherapy.  
 OS Synthetic.  
 PN EP-700929-A2.  
 PD 13-MAR-1996.  
 PE 08-SEP-1995; 306295.  
 PR 10-SEP-1994; JP-242137.  
 PR 14-JUL-1995; JP-200221.  
 PR 14-JUL-1995; JP-200204.  
 PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.  
 PI Hino K, Saito S, Taniguchi Y.  
 DR WPI: 96-140976/15.  
 PT New peptide(s) derived from cedar pollen allergens - activate  
 PT allergen-specific T-cells, but not allergen-specific IGE antibodies,  
 PS used for treating cedar pollinosis  
 PS Claim 4; Page 28; 36pp; English.  
 CC Synthetic peptides based on portions of cedar pollen allergens A  
 CC (R81586) and B (R81587) were tested for their ability to activate  
 CC cedar allergen-specific T-cells, but not allergen-specific IGE  
 CC antibodies. 6 peptides (R81580-R81585) were identified as T-cell  
 CC epitopes. These peptides, plus subsequences (R81573-79) essential  
 CC for T-cell recognition, and homologous peptides (R81588-96) can  
 CC be used as immunotherapeutic agents to treat or prevent cedar  
 CC pollinosis, avoiding side-effects such as anaphylaxis.  
 SQ Sequence 17 AA;

Query Match 19.5%; Score 111; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 2.03e-01;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 KVDGIITAYONPASMWK 16  
 :|||||  
 QY 65 RVDGIITAYONPASMWK 80

RESULT 8  
 ID R97884 standard; peptide; 15 AA.  
 AC R97884;  
 DT 16-AUG-1996 (first entry)  
 DE Japan cedar pollen mature allergen Cry j II amino acids 66-80.  
 KW Allergen; epitope; overlapping peptide; Cry j II; cedar pollen;  
 KW sugi pollinosis; diagnosis; treatment.  
 OS Cryptomeria japonica.  
 PN J08047392-A.  
 PD 20-FEB-1996.  
 PE 07-NOV-1994; 297840.  
 PR 05-NOV-1993; JP-276773.  
 PR 26-MAY-1994; JP-134868.  
 PA (MEIP) MEIJI MILK PROD CO LTD.  
 DR WPI: 96-166249/17.  
 PT Japan cedar pollen allergen Cry j II epitope - comprises at least  
 PT part of specified 460 amino acid protein  
 PS Claim 8; Fig 3; 17pp; Japanese.  
 CC R97871-R97960 are overlapping peptides used for the epitope mapping  
 CC of the Japan cedar pollen allergen Cry j II. Cry j II and allergenic  
 CC peptides of it are useful in the diagnosis, prevention and treatment  
 CC of Sugi pollinosis, the allergic reaction to Japan cedar pollen.  
 CC Significant regions of the full peptide were identified using the  
 CC overlapping peptides of the full peptide derived from a Cry j II  
 CC antigen-specific T cell line. Amino acids 66-80 (R97884) and 186-200  
 CC (R978808) of the full mature 460 amino acid allergen are the most  
 CC allergenic of the 90 peptides tested.

SQ Sequence 15 AA;  
 Query Match 18.8%; Score 107; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4.34e-01;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 VDGIIITAYONPASMWK 15  
 :|||||  
 QY 66 VDGIIITAYONPASMWK 80

RESULT 9  
 ID W57760 standard; peptide; 15 AA.  
 AC W57760;  
 DT 17-SEP-1998 (first entry)  
 DE Residues 66-80 of Cry j 2.  
 KW Cry j 2; Japanese cedar pollen antigen; allergy; immunotherapy;  
 KM HLA class II molecule.  
 OS Cryptomeria japonica.  
 PN W09820902-A1.  
 PD 22-MAY-1998.  
 PE 12-NOV-1997; J04129.  
 PR 13-NOV-1996; JP-302053.  
 PA (MEIP) MEIJI MILK PROD CO LTD.  
 PI Dairiki K, Kuno K, Kume A, Sone T;  
 DR WPI: 98-297617/26.  
 PT Peptides derived from Japanese cedar pollen antigens are  
 PT immunotherapeutic agents - useful for allergy treatment and typing  
 PT HLA class II molecules in allergy sufferers  
 PS Claim 12; Page 30; 50pp; Japanese.  
 CC This sequence represents residues 66-80 of the Cry j 2 protein, and  
 CC is a peptide of the invention. The peptides are derived from Japanese  
 CC cedar pollen antigens, and are used as immunotherapeutic agents in the  
 CC treatment of allergy. The peptides can be used for identification and  
 CC typing of the particular HLA class II molecules in an allergy sufferer,  
 CC and also for peptide immunotherapy of an allergy. Using these peptides  
 CC the immunotherapy can be targeted more specifically to the requirements  
 CC of the individual patient, allowing more effective treatment of an  
 CC allergy, including those patients for whom treatment with a conventional  
 CC immunotherapeutic agent is ineffective.  
 SQ Sequence 15 AA;

Query Match 18.8%; Score 107; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4.34e-01;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 VDGIIITAYONPASMWK 15  
 :|||||  
 QY 66 VDGIIITAYONPASMWK 80

RESULT 10  
 ID W80350 standard; peptide; 47 AA.  
 AC W80350;  
 DT 11-JAN-1999 (first entry)  
 DE Sugi allergen protein Cryj1 derived epitope for T cells.  
 KW T cell epitope; sugi allergen proteins Cryj1; Cryj2; treatment;  
 KW sugi-pollinosis; allergic reaction; pollen.  
 OS Synthetic.  
 PN J10259198-A.  
 PD 29-SEP-1998.  
 PE 22-DEC-1997; 353448.  
 PR 24-DEC-1996; JP-343441.  
 PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.  
 PI (SANY) SANKYO CO LTD.  
 DR WPI: 98-577037/49.  
 PT A linked T cell epitope peptide - used for the treatment of  
 PT sugi-pollinosis  
 PS Claim 10; Page 5; 21pp; Japanese.  
 CC W80339-58 represent epitopes for T cells, derived from the sugi allergen  
 CC proteins Cryj1 (W80339-44), W80350-53 and W80356-58) and Cryj2 (W80345-49  
 CC and W80354-55). The peptides are useful for the treatment of  
 CC sugi-pollinosis, an allergic reaction of the body to pollen.

SQ Sequence 47 AA:

Query Match 18.8%; Score 107; DB 1; Length 47;  
 Best Local Similarity 65.6%; Pred. No. 4,34e-01;  
 Matches 21; Conservative 4; Mismatches 5; Indels 2; Gaps 2;

DB 13 FASKNFHLQKNTMKTVAENQFKLTSKIAS 44  
 |||||  
 OY 34 FASKNFHLQKNTIGTRIS-L-KLTSKIAS 63

RESULT 11  
 ID W80356 standard; peptide; 47 AA.

AC W80356;  
 DT 11-JAN-1999 (first entry)  
 DE Sugl allergen protein Cryj1 derived epitope for T cells.  
 KW T cell epitope; sugl allergen proteins Cryj1; Cryj2; treatment;  
 KM sugl-pollinosis; allergic reaction; pollen.  
 OS Synthetic.  
 PN J10259198-A.  
 PD 29-SEP-1998.  
 PE 22-DEC-1997; 353448.  
 PR 24-DEC-1996; JP-343441.  
 PA (HAYB) HAYASHIBARA SEIBUNSU KAGAKU.  
 PI WPI: 96-57703/49.  
 DR A linked T cell epitope peptide - used for the treatment of  
 PT sugl-pollinosis  
 PS Claim 10; Page 5; 21pp; Japanese.  
 CC W80339-58 represent epitopes for T cells, derived from the sugl allergen  
 CC proteins Cryj1 (W80339-44; W80350-53 and W80356-58) and Cryj2 (W80345-49  
 CC and W80354-55). The peptides are useful for the treatment of  
 CC sugl-pollinosis, an allergic reaction of the body to pollen.  
 SQ Sequence 47 AA;

Query Match 18.6%; Score 106; DB 1; Length 47;  
 Best Local Similarity 69.7%; Pred. No. 5,24e-01;  
 Matches 23; Conservative 2; Mismatches 5; Indels 3; Gaps 2;

DB 1 FASKNFHLQKNTGIIAAYONPASKMLTSKIAS 33  
 |||||  
 OY 34 FASKNFHLQKNT-IGT-GRISLKLTSKIAS 63

RESULT 12  
 ID W80342 standard; peptide; 35 AA.  
 AC W80342;  
 DT 11-JAN-1999 (first entry)  
 DE Sugl allergen protein Cryj1 derived epitope for T cells.  
 KW T cell epitope; sugl allergen proteins Cryj1; Cryj2; treatment;  
 KM sugl-pollinosis; allergic reaction; pollen.  
 OS Synthetic.  
 PN J10259198-A.  
 PD 29-SEP-1998.  
 PE 22-DEC-1997; 353448.  
 PR 24-DEC-1996; JP-343441.  
 PA (HAYB) HAYASHIBARA SEIBUNSU KAGAKU.  
 PI WPI: 96-57703/49.  
 DR A linked T cell epitope peptide - used for the treatment of  
 PT sugl-pollinosis  
 PS Claim 10; Page 5; 21pp; Japanese.  
 CC W80339-58 represent epitopes for T cells, derived from the sugl allergen  
 CC proteins Cryj1 (W80339-44; W80350-53 and W80356-58) and Cryj2 (W80345-49  
 CC and W80354-55). The peptides are useful for the treatment of  
 CC sugl-pollinosis, an allergic reaction of the body to pollen.  
 SQ Sequence 35 AA;

Query Match 18.1%; Score 103; DB 1; Length 35;  
 Best Local Similarity 66.7%; Pred. No. 9,20e-01;  
 Matches 22; Conservative 2; Mismatches 6; Indels 3; Gaps 2;

DB 1 FASKNFHLQKNTGIIAAYONPASKMLTSKIAS 33

OY 34 FASKNFHLQKNT-IGT-GRISLKLTSKIAS 63  
 |||||

RESULT 13  
 ID W57764 standard; peptide; 15 AA.

AC W57764;  
 DT 17-SEP-1998 (first entry)  
 DE Residues 186-200 of Cry j 2.  
 KW Cry j 2; Japanese cedar pollen antigen; allergy; immunotherapy;  
 KM HLA class II molecule.  
 OS Cryptomeria japonica.  
 PN W06820902-A1.  
 PD 22-MAY-1998.  
 PE 12-NOV-1997; J04129.  
 PR 13-NOV-1996; JP-302053.  
 PA (MEIP) MEIJI MILK PROD CO LTD.  
 PI Dairiki K, Kuno K, Kume A, Sone T;  
 DR WPI: 96-297617/26.  
 PT Peptides derived from Japanese cedar pollen antigens are  
 PT immunotherapeutic agents - useful for allergy treatment and typing  
 PT HLA Class II molecules in allergy sufferers  
 PS Claim 12; Page 31; 50pp; Japanese.  
 CC This sequence represents residues 186-200 of the Cry j 2 protein, and  
 CC is a peptide of the invention. The peptides are derived from Japanese  
 CC cedar pollen antigens, and are used as immunotherapeutic agents in the  
 CC treatment of allergy. The peptides can be used for identification and  
 CC typing of the particular HLA class II molecules in an allergy sufferer,  
 CC and also for peptide immunotherapy of an allergy. Using these peptides  
 CC the immunotherapy can be targeted more specifically to the requirements  
 CC of the individual patient, allowing more effective treatment of an  
 CC allergy, including those patients for whom treatment with a conventional  
 CC immunotherapeutic agent is ineffective.  
 SQ Sequence 15 AA;

Query Match 17.2%; Score 98; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2,33e+00;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 ASKNFHLQKNTIGTG 15  
 |||||  
 OY 35 ASKNFHLQKNTIGTG 49

RESULT 14  
 ID R97908 standard; peptide; 15 AA.  
 AC R97908;  
 DT 16-AUG-1996 (first entry)  
 DE Japan cedar pollen mature allergen Cry j II amino acids 186-200.  
 KW Allergen; epitope; overlapping peptide; Cry j II; cedar pollen;  
 KM sugl pollinosis; diagnosis; treatment.  
 OS Cryptomeria japonica.  
 PN J08047392-A.  
 PD 20-FEB-1996.  
 PE 07-NOV-1994; 297840.  
 PR 05-NOV-1993; JP-276773.  
 PR 26-MAY-1994; JP-134868.  
 PA (MEIP) MEIJI MILK PROD CO LTD.  
 PI WPI: 96-166249/17.  
 DR Japan cedar pollen allergen Cry j II epitope - comprises at least  
 PT part of specified 460 amino acid protein  
 PS Claim 8; Fig 4; 17pp; Japanese.  
 CC R97871-R97960 are overlapping peptides used for the epitope mapping  
 CC of the Japan cedar pollen allergen Cry j II. Cry j II and allergenic  
 CC peptides of it are useful in the diagnosis, prevention and treatment  
 CC of sugl pollinosis, the allergic reaction to Japan cedar pollen.  
 CC Significant regions of the allergen were identified using the  
 CC overlapping peptides of the full epitope derived from a Cry j II  
 CC antigen-specific T cell line. Amino acids 66-80 (R97884) and 186-200  
 CC (R978908) of the full mature 460 amino acid allergen are the most  
 CC allergenic of the 90 peptides tested.  
 SQ Sequence 15 AA;



Query Match 17.2%; Score 98; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.33e+00;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 ASKNFHLQKNTGTG 15  
 |||||||  
 QY 35 ASKNFHLQKNTGTG 49

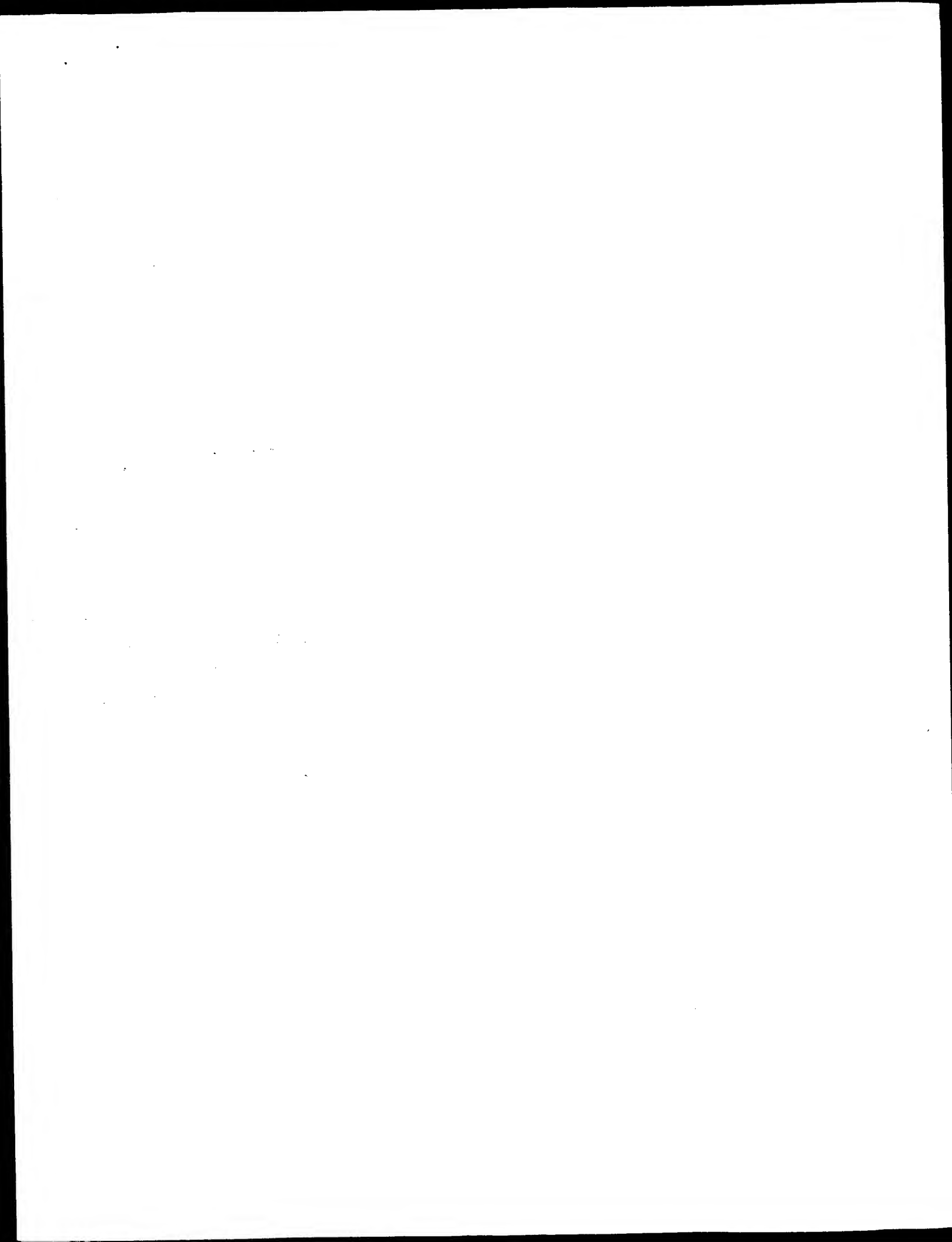
## RESULT 15

ID R97907 standard; peptide; 15 AA.  
 AC R97907:  
 DT 16-AUG-1996 (first entry)  
 DE Japan cedar pollen mature allergen Cry j II amino acids 181-195.  
 KW Allergen; epitope; overlapping peptide; Cry j II; cedar pollen;  
 KM Sugi pollinosis; diagnosis; treatment.  
 OS Cryptomeria japonica.  
 PN J08047392-A.  
 PD 20-FEB-1996:  
 PR 07-NOV-1994; 297840.  
 PR 05-NOV-1993; JP-276773.  
 PR 26-MAY-1994; JP-134868.  
 PA (MEIP ) MEIJI MILK PROD CO LTD.  
 DR WPI; 96-166249/17.  
 PT Japan cedar pollen allergen Cry j II epitope - comprises at least  
 PS part of specified 460 amino acid protein  
 CS Claim 8; Fig 4; 17pp; Japanese.  
 CC R97871-R97960 are overlapping peptides used for the epitope mapping  
 CC of the Japan cedar pollen allergen Cry j II. Cry j II and allergenic  
 CC peptides of it are useful in the diagnosis, prevention and treatment  
 CC of Sugi pollinosis, the allergic reaction to Japan cedar pollen.  
 CC Significant regions of the allergen were identified using the  
 CC overlapping peptides of the full epitope derived from a Cry j II  
 CC antigen-specific T cell line. Amino acids 66-80 (R97884) and 186-200  
 CC (R978908) of the full mature 460 amino acid allergen are the most  
 CC allergenic of the 90 peptides tested.  
 SQ Sequence 15 AA;

Query Match 17.2%; Score 98; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.33e+00;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2 IDIFASKNFHLQKN 15  
 |||||||  
 QY 31 IDIFASKNFHLQKN 44

Search completed: Mon Jun 19 15:57:41 2000  
 Job time : 14 secs.



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WIPERH  
(TM)  
\*\*\*\*\*

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Mpsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Jun 19 15:57:00 2000; MasPar time 9.23 Seconds

Tabular output not generated. 408.972 Million cell updates/sec

Title: >US-09-142-524A-1

Description: (1-80) from US09142524A.pep

Perfect Score: 569

Sequence: 1 MKVYVAFNQFGPNRRVFTKR.....IASRRVDGIIAAYONPASWK 80

Scoring table:

PAM 150  
Gap 11

Searched: 142080 segs, 47172406 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries  
Maximum DB seq length 80

Database: p1r62

1:p1r1 2:p1r2 3:p1r3 4:p1r4

Statistics: Mean 39.829; Variance 80.867; scale 0.493

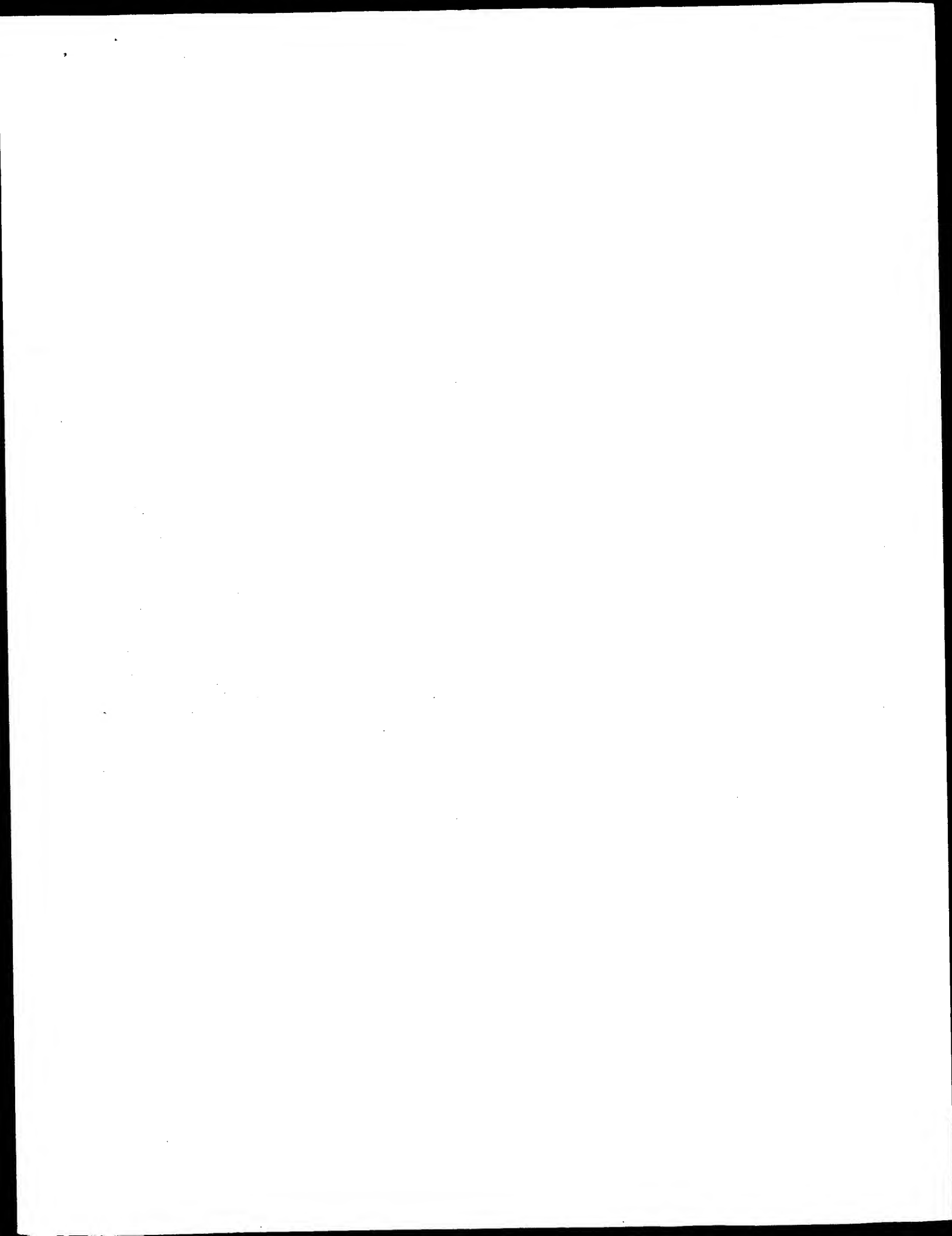
Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Query	No.	Score	Match	Length	DB	ID	Description	Pred.	No.
-----										

No matches found.

Search completed: Mon Jun 19 15:57:10 2000  
Job time : 10 secs.



\*\*\*\*\*  
 W P E R L H  
 (TM)  
 \*\*\*\*\*

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Mpsrch\_dp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Jun 19 15:55:43 2000; MasPar time 5.66 Seconds

Tabular output not generated. 430.118 Million cell updates/sec

Title: >US-09-142-524A-1  
 Description: (1-80) from US09142524A.pep  
 Perfect Score: 569  
 Sequence: 1 MKVTVAFNQFGPNRRVFIK.....IASRRVDCIIAAYONPASWK 80

Scoring table: PAM 150  
 Gap 11

Searched: 83857 seqs, 30454973 residues

Post-processing: Minimum Match 0%  
 Listing first 45 summaries  
 Maximum DB seq length 80

Database: swiss-prot38  
 1:swissprot

Statistics: Mean 40.706; Variance 73.263; scale 0.556

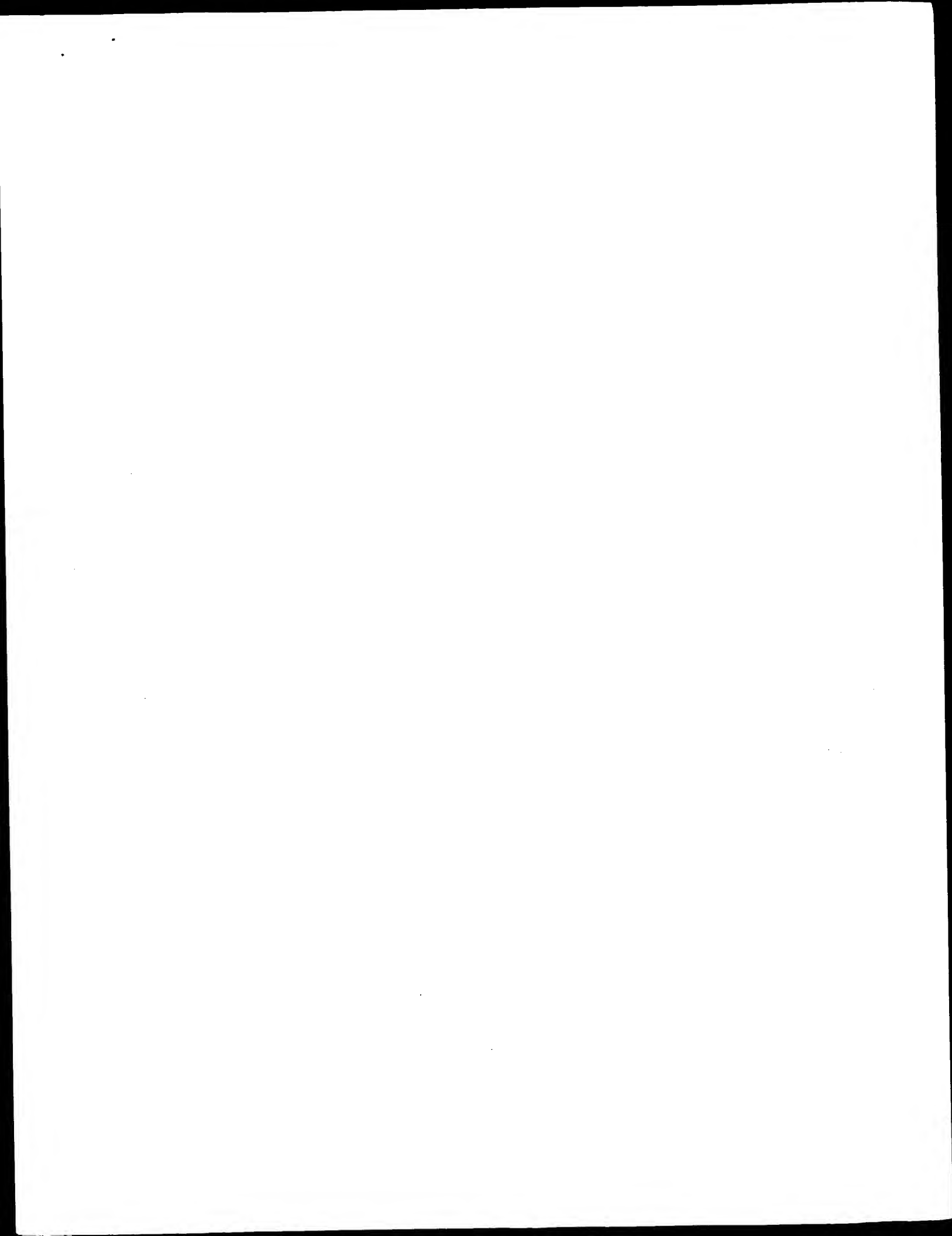
Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

# SUMMARIES

Result	Query					
No.	Score	Match	length	ID	Description	Pred. No.
-----						

No matches found.

Search completed: Mon Jun 19 15:56:03 2000  
 Job time : 20 secs.



WIPERH (TM)

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Mpsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Jun 19 15:56:19 2000; MasPar time 14.21 Seconds

Tabular output not generated. 390.261 Million cell updates/sec

Title: >US-09-142-524A-1

Description: (1-80) from US09142524A.pep

Perfect Score: 569

Sequence: 1 MKVYVAFNQFGPNRRVFTR.....IASRRVDGIITAYQNPASWK 80

Scoring table: PAM 150

Gap 11

Searched: 225878 segs, 69334122 residues

Post-processing: Minimum Match 08

Listing first 45 summaries

Maximum DB seq length 80

Database:

sptrembl12

1:sp\_archaea 2:sp\_bacteria 3:sp\_fungi 4:sp\_human

5:sp\_invertebrate 6:sp\_mammal 7:sp\_mhc 8:sp\_organelle

9:sp\_phage 10:sp\_plant 11:sp\_rodent 12:sp\_unclassified

13:sp\_vertebrate 14:sp\_virus

Statistics: Mean 39.247; Variance 71.415; scale 0.550

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Query	Match	Length	ID	Description	Pred. No.
No. score	Match	Length	ID	Description	Pred. No.	

No matches found.

Search completed: Mon Jun 19 15:56:42 2000  
 Job time : 23 secs.

